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OM protein - protein search, using sw model

Run on: December 12, 2003, 12:14:52 ; Search time 48.1424 Seconds
(without alignments)
1016.022 Million cell updates/sec

Title: US-10-047-264A-4
Perfect score: 1432
Sequence: 1 MPMKHCFLGLISFFLTGVA.....YQPLDRSRSERCVEIP 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues
Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1432 | 100.0 | 263 | 12 | US-10-047-264A-4 |
| 2 | 1432 | 100.0 | 263 | 12 | US-10-293-832-28 |
| 3 | 1432 | 100.0 | 263 | 12 | US-10-312-088-42 |
| 4 | 1428 | 99.7 | 263 | 11 | US-09-961-404-6 |
| 5 | 1218 | 85.1 | 231 | 9 | US-09-728-911-2 |
| 6 | 1218 | 85.1 | 231 | 10 | US-09-949-192-6 |
| 7 | 1218 | 85.1 | 231 | 11 | US-09-961-404-4 |
| 8 | 1218 | 85.1 | 231 | 12 | US-10-237-496-114 |
| 9 | 1218 | 85.1 | 231 | 12 | US-10-242-074-114 |
| 10 | 1218 | 85.1 | 231 | 12 | US-10-242-505-114 |
| 11 | 1218 | 85.1 | 231 | 12 | US-10-242-574-114 |
| 12 | 1218 | 85.1 | 231 | 12 | US-10-243-261-114 |
| 13 | 1218 | 85.1 | 231 | 12 | US-10-243-282-114 |
| 14 | 1218 | 85.1 | 231 | 12 | US-10-243-402-114 |
| 15 | 1218 | 85.1 | 231 | 12 | US-10-243-431-114 |

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| 16 | 1218 | 85.1 | 231 | 12 | US-10-245-164-114 |
| 17 | 1218 | 85.1 | 231 | 12 | US-09-746-375-33 |
| 18 | 1218 | 85.1 | 231 | 12 | US-10-047-264A-2 |
| 19 | 1218 | 85.1 | 231 | 12 | US-10-047-264A-35 |
| 20 | 1218 | 85.1 | 231 | 12 | US-10-244-972-114 |
| 21 | 1218 | 85.1 | 231 | 12 | US-10-197-942-114 |
| 22 | 1218 | 85.1 | 231 | 12 | US-10-293-832-25 |
| 23 | 1218 | 85.1 | 231 | 12 | US-10-238-196-114 |
| 24 | 1218 | 85.1 | 231 | 12 | US-10-245-013-114 |
| 25 | 1218 | 85.1 | 231 | 12 | US-10-312-088-41 |
| 26 | 1218 | 85.1 | 231 | 15 | US-10-245-103-114 |
| 27 | 1218 | 85.1 | 231 | 15 | US-10-245-107-114 |
| 28 | 1218 | 85.1 | 231 | 15 | US-10-245-143-114 |
| 29 | 1218 | 85.1 | 231 | 15 | US-10-245-771-114 |
| 30 | 1218 | 85.1 | 231 | 15 | US-10-245-851-114 |
| 31 | 1218 | 85.1 | 231 | 15 | US-10-245-883-114 |
| 32 | 1218 | 85.1 | 231 | 15 | US-10-237-535-114 |
| 33 | 1218 | 85.1 | 231 | 15 | US-10-238-183-114 |
| 34 | 1218 | 85.1 | 231 | 15 | US-10-238-283-114 |
| 35 | 1218 | 85.1 | 231 | 15 | US-10-238-370-114 |
| 36 | 1218 | 85.1 | 231 | 15 | US-10-245-055-114 |
| 37 | 1218 | 85.1 | 231 | 15 | US-10-245-147-114 |
| 38 | 1218 | 85.1 | 231 | 15 | US-10-245-730-114 |
| 39 | 1218 | 85.1 | 231 | 15 | US-10-245-739-114 |
| 40 | 1218 | 85.1 | 231 | 15 | US-10-246-210-114 |
| 41 | 1218 | 85.1 | 231 | 15 | US-10-239-196-114 |
| 42 | 1218 | 85.1 | 231 | 15 | US-10-090-365-2 |
| 43 | 1218 | 85.1 | 231 | 15 | US-10-243-024-114 |
| 44 | 1218 | 85.1 | 231 | 15 | US-10-243-409-114 |
| 45 | 1218 | 85.1 | 231 | 15 | US-10-245-621-114 |

ALIGNMENTS

RESULT 1
US-10-047-264A-4
; Sequence 4, Application US/10047264A
; Publication No. US20030170839A1
; GENERAL INFORMATION:
; APPLICANT: Fouser, Lynette
; APPLICANT: Liu, Wei
; APPLICANT: Deng, Bijia
; TITLE OF INVENTION: TYPE 2 CYTOKINE RECEPTOR AND NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 22058-532
; CURRENT APPLICATION NUMBER: US/10/047,264A
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/261442
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/267021
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/270835
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 263
; TYPE: PRT
; ORGANISM: human
US-10-047-264A-4

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|-----------------------|-----------------|-----------------------------|--------------------------|----------------|
| Query Match | 100.0%; | Score 1432; | DB 12; | Length 263; |
| Best local Similarity | 100.0%; | Pred. No. 4e-136; | | |
| Matches 263; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | MPMKHCFLGLISFFLTGVA | QSTHESLKPQVQFSRNFHNLQWPG | RGALTGNSSVY 60 |
| Db | 1 | MPMKHCFLGLISFFLTGVA | QSTHESLKPQVQFSRNFHNLQWPG | RGALTGNSSVY 60 |
| Qy | 61 | FVQYKMFSCSMKSHQKPSGCWHQISCN | PPGCRITLAKYQGORWKNKEDC | WGTOELSCDL 120 |
| Db | 61 | FVQYKMFSCSMKSHQKPSGCWHQISCN | PPGCRITLAKYQGORWKNKEDC | WGTOELSCDL 120 |

QY 121 TSETSDIOEPYGRVRAASAGSYSEWSMTPTPTPWETKIDPPVNNITQVNGSLVILHA 180
DB 121 TSETSDIOEPYGRVRAASAGSYSEWSMTPTPTPWETKIDPPVNNITQVNGSLVILHA 180
QY 181 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
DB 181 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
QY 241 AEIYQPMDDRORSERCEVEIP 263
DB 241 AEIYQPMDDRORSERCEVEIP 263

RESULT 2

US-10-293-832-28
; Sequence 28, Application US/10293832
; Publication No. US20030180752A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Wei
; APPLICANT: Fouser, Lynette
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: TYPE 2 CYTOKINE RECEPTOR AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 22058-546
; CURRENT APPLICATION NUMBER: US/10/293,832
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/332,366
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 28
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-832-28

Query Match 100.0%; Score 1432; DB 12; Length 263;
Best Local Similarity 100.0%; Pred. No. 4e-138;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPMKHFGLFLISFLTGAGTOSTHSLKQPVQFOSRNFHNLQWPGRALTGNSVY 60
DB 1 MPMKHFGLFLISFLTGAGTOSTHSLKQPVQFOSRNFHNLQWPGRALTGNSVY 60
QY 61 FVOYKIMFSCMSKSHQKPSGCWQHISCNPFPGCTRLAKYQORQWKNKDCWGTOLSCDL 120
DB 61 FVOYKIMFSCMSKSHQKPSGCWQHISCNPFPGCTRLAKYQORQWKNKDCWGTOLSCDL 120
QY 121 TSETSDIOEPYGRVRAASAGSYSEWSMTPTPTPWETKIDPPVNNITQVNGSLVILHA 180
DB 121 TSETSDIOEPYGRVRAASAGSYSEWSMTPTPTPWETKIDPPVNNITQVNGSLVILHA 180
QY 181 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
DB 181 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
QY 241 AEIYQPMDDRORSERCEVEIP 263
DB 241 AEIYQPMDDRORSERCEVEIP 263

RESULT 3

US-10-312-088-42
; Sequence 42, Application US/10312088
; Publication No. US20030219862A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Cogswell, John P.
; APPLICANT: Kabnic, Karen S.
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Martensen, Shelby A.
; APPLICANT: Murdock, Paul R.
; APPLICANT: Smith, Randall F.

; APPLICANT: Strum, Jay C.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Xie, Qing
; APPLICANT: Rizni, Safia K.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GFS0029
; CURRENT APPLICATION NUMBER: US/10/312,088
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/19929
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,161
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/213,156
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-088-42

Query Match 100.0%; Score 1432; DB 12; Length 263;
Best Local Similarity 100.0%; Pred. No. 4e-138;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPMKHFGLFLISFLTGAGTOSTHSLKQPVQFOSRNFHNLQWPGRALTGNSVY 60
DB 1 MPMKHFGLFLISFLTGAGTOSTHSLKQPVQFOSRNFHNLQWPGRALTGNSVY 60
QY 61 FVOYKIMFSCMSKSHQKPSGCWQHISCNPFPGCTRLAKYQORQWKNKDCWGTOLSCDL 120
DB 61 FVOYKIMFSCMSKSHQKPSGCWQHISCNPFPGCTRLAKYQORQWKNKDCWGTOLSCDL 120
QY 121 TSETSDIOEPYGRVRAASAGSYSEWSMTPTPTPWETKIDPPVNNITQVNGSLVILHA 180
DB 121 TSETSDIOEPYGRVRAASAGSYSEWSMTPTPTPWETKIDPPVNNITQVNGSLVILHA 180
QY 181 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
DB 181 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
QY 241 AEIYQPMDDRORSERCEVEIP 263
DB 241 AEIYQPMDDRORSERCEVEIP 263

RESULT 4

US-09-961-404-6
; Sequence 6, Application US/09961404
; Publication No. US20030022827A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: SABAT, ROBERT
; APPLICANT: ASADULLAH, KHUSRU
; APPLICANT: TOSCHI, LUISSELLA
; TITLE OF INVENTION: THREE NEW MEMBERS OF THE CYTOKINE RECEPTOR
; FILE REFERENCE: SCH-1788
; CURRENT APPLICATION NUMBER: US/09/961,404
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-404-6

Query Match 99.7%; Score 1428; DB 11; Length 263;
Best Local Similarity 99.6%; Pred. No. 1e-137;
Matches 262; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

12/13/06 60/254,896
* SEQ ID: 6 miss aa, 67-98
seq

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Db 1 MNPXKCFGLFLISFFLTGAGTOSTHESLKPQVQFQSRNFHNLQWQPGRALTGNSVY 60
QY 61 FVOYKIMFSCSKSHQKPSGCHQHSNFGCTLAKYQORQWKNKEDCWGTQELSDDL 120
Db 61 FVOYKIMFSCSKSHQKPSGCHQHSNFGCTLAKYQORQWKNKEDCWGTQELSDDL 120
QY 121 TSETSDIQEPYGRVRAASAGSYSEWSMTFRPTPWMTETKIDPPVMNITQVNGSLVILHA 180
Db 121 TSETSDIQEPYGRVRAASAGSYSEWSMTFRPTPWMTETKIDPPVMNITQVNGSLVILHA 180
QY 181 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
Db 181 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
QY 241 AEIYQPMMLDRRSORSEERCVEIP 263
Db 241 AEIYQPMMLDRRSORSEERCVEIP 263

RESULT 5

US-09-728-911-2

; Sequence 2, Application US/09728911

; Patent No. US20020012669A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Xu, Wenfeng

; APPLICANT: Kindevogel, Wayne

; APPLICANT: Chen, Zhi

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 99-93

; CURRENT APPLICATION NUMBER: US/09/728,911

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: US 60/169,049

; PRIOR FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: US 60/232,219

; PRIOR FILING DATE: 2000-09-13

; PRIOR APPLICATION NUMBER: US 60/244,610

; PRIOR FILING DATE: 2000-10-31

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 231

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-728-911-2

Query Match 85.1%; Score 1218; DB 9; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MNPXKCFGLFLISFFLTGAGTOSTHESLKPQVQFQSRNFHNLQWQPGRALTGNSVY 60
Db 1 MNPXKCFGLFLISFFLTGAGTOSTHESLKPQVQFQSRNFHNLQWQPGRALTGNSVY 60
QY 61 FVOYKIMFSCSKSHQKPSGCHQHSNFGCTLAKYQORQWKNKEDCWGTQELSDDL 120
Db 61 FVOYKI-----YQORQWKNKEDCWGTQELSDDL 88
QY 121 TSETSDIQEPYGRVRAASAGSYSEWSMTFRPTPWMTETKIDPPVMNITQVNGSLVILHA 180
Db 89 TSETSDIQEPYGRVRAASAGSYSEWSMTFRPTPWMTETKIDPPVMNITQVNGSLVILHA 148
QY 181 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
Db 149 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 208
QY 241 AEIYQPMMLDRRSORSEERCVEIP 263
Db 209 AEIYQPMMLDRRSORSEERCVEIP 231

RESULT 6

US-09-949-192-6

; Sequence 6, Application US/09949192

; Patent No. US20020142292A1

; GENERAL INFORMATION:

; APPLICANT: Parham, Christi L.

; APPLICANT: Gorman, Daniel L.

; APPLICANT: Kurata, Hirokazu

; APPLICANT: Arai, Naoko

; APPLICANT: Sana, Theodore R.

; APPLICANT: Mattoon, Jeanine D.

; APPLICANT: Murphy, Erin E.

; APPLICANT: Savkoor, Chetan

; APPLICANT: Grein, Jeffery

; APPLICANT: Smith, Kathleen M.

; APPLICANT: McClanahan, Terrill K.

; TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS AND METHODS

; FILE REFERENCE: DX01169K

; CURRENT APPLICATION NUMBER: US/09/949,192

; CURRENT FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: 60/231,267

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 231

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-949-192-6

Query Match 85.1%; Score 1218; DB 10; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MNPXKCFGLFLISFFLTGAGTOSTHESLKPQVQFQSRNFHNLQWQPGRALTGNSVY 60
Db 1 MNPXKCFGLFLISFFLTGAGTOSTHESLKPQVQFQSRNFHNLQWQPGRALTGNSVY 60
QY 61 FVOYKIMFSCSKSHQKPSGCHQHSNFGCTLAKYQORQWKNKEDCWGTQELSDDL 120
Db 61 FVOYKI-----YQORQWKNKEDCWGTQELSDDL 88
QY 121 TSETSDIQEPYGRVRAASAGSYSEWSMTFRPTPWMTETKIDPPVMNITQVNGSLVILHA 180
Db 89 TSETSDIQEPYGRVRAASAGSYSEWSMTFRPTPWMTETKIDPPVMNITQVNGSLVILHA 148
QY 181 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
Db 149 PNLPRYQKKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 208
QY 241 AEIYQPMMLDRRSORSEERCVEIP 263
Db 209 AEIYQPMMLDRRSORSEERCVEIP 231

RESULT 7

US-09-961-404-4

; Sequence 4, Application US/09961404

; Publication No. US20030022827A1

; GENERAL INFORMATION:

; APPLICANT: WEISS, BERTRAM

; APPLICANT: SABAT, ROBERT

; APPLICANT: ASADULLAH, KHUSRU

; APPLICANT: TOSCHI, LUISSELLA

; TITLE OF INVENTION: THREE NEW MEMBERS OF THE CYTOKINE RECEPTOR

; FILE REFERENCE: SCH-1788

; CURRENT APPLICATION NUMBER: US/09/961,404

; CURRENT FILING DATE: 2001-09-25

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 231

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-404-4

Query Match      85.1%; Score 1218; DB 11; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPPKHCFGLFLISFFLTGAGTQSTHESLKPQVQFOSRNFHNILOQPGALTGNSVY 60
DB 1 MPPKHCFGLFLISFFLTGAGTQSTHESLKPQVQFOSRNFHNILOQPGALTGNSVY 60
QY 61 FVQYKIMFSCMSKSSHQKPSGCWQHISCNFPGCRTLAKYQORQWKNKEDCWGTQELSDDL 120
DB 61 FVQYKI-----YQORQWKNKEDCWGTQELSDDL 88
QY 121 TSETSDIOEPYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVILHA 180
DB 89 TSETSDIOEPYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVILHA 148
QY 181 PNLPRYQKEKNVSIEDYVELLYRVFIINNSLEKEQKYEGAHRAVEIEALTPHSSYCVV 240
DB 149 PNLPRYQKEKNVSIEDYVELLYRVFIINNSLEKEQKYEGAHRAVEIEALTPHSSYCVV 208
QY 241 AEIYQPMLDRRSQRSEERCVEIP 263
DB 209 AEIYQPMLDRRSQRSEERCVEIP 231

RESULT 8
US-10-237-496-114
; Sequence 114, Application US/10237496
; Publication No. US20030138896A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C4
; CURRENT APPLICATION NUMBER: US/10/237,496
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO 114
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-237-496-114

Query Match      85.1%; Score 1218; DB 12; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPPKHCFGLFLISFFLTGAGTQSTHESLKPQVQFOSRNFHNILOQPGALTGNSVY 60
DB 1 MPPKHCFGLFLISFFLTGAGTQSTHESLKPQVQFOSRNFHNILOQPGALTGNSVY 60
QY 61 FVQYKIMFSCMSKSSHQKPSGCWQHISCNFPGCRTLAKYQORQWKNKEDCWGTQELSDDL 120
DB 61 FVQYKI-----YQORQWKNKEDCWGTQELSDDL 88
QY 121 TSETSDIOEPYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVILHA 180
DB 89 TSETSDIOEPYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVILHA 148
QY 181 PNLPRYQKEKNVSIEDYVELLYRVFIINNSLEKEQKYEGAHRAVEIEALTPHSSYCVV 240
DB 149 PNLPRYQKEKNVSIEDYVELLYRVFIINNSLEKEQKYEGAHRAVEIEALTPHSSYCVV 208
QY 241 AEIYQPMLDRRSQRSEERCVEIP 263
DB 209 AEIYQPMLDRRSQRSEERCVEIP 231

RESULT 9
US-10-242-074-114
; Sequence 114, Application US/10242074
; Publication No. US20030138897A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C9
; CURRENT APPLICATION NUMBER: US/10/242,074
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
```

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 114
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-074-114

Query Match      85.1%; Score 1218; DB 12; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPPKHCFLGFLISFFLTGTAGTQSTHESLKQPVQFQSRNFHNILOWQGRALTGNSVY 60
Db 1 MPPKHCFLGFLISFFLTGTAGTQSTHESLKQPVQFQSRNFHNILOWQGRALTGNSVY 60
QY 61 FVQYKIMFSCSMKSSHQKPSGCWHISCNFPGCRTLAKYQGRQWKNEKDCWGTQELSCDL 120
Db 61 FVQYKI-----YGRQWKNEKDCWGTQELSCDL 88
QY 121 TSETSDIQBPYGRVRAASAGSYSEWSMTPRFTPPWNETKIDPPVMNITQVNGSLVILHA 180
Db 89 TSETSDIQBPYGRVRAASAGSYSEWSMTPRFTPPWNETKIDPPVMNITQVNGSLVILHA 148
QY 181 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 240
Db 149 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 208
QY 241 ABIYQPMLEDRRSQSRSEECVEIP 263
Db 209 ABIYQPMLEDRRSQSRSEECVEIP 231

RESULT 10
US-10-242-505-114
; Sequence 114, Application US/10242505
; Publication No. US20030138898A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C25
; CURRENT APPLICATION NUMBER: US/10/242,505
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
```

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; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 114
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-505-114

Query Match      85.1%; Score 1218; DB 12; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPPKHCFLGFLISFFLTGTAGTQSTHESLKQPVQFQSRNFHNILOWQGRALTGNSVY 60
Db 1 MPPKHCFLGFLISFFLTGTAGTQSTHESLKQPVQFQSRNFHNILOWQGRALTGNSVY 60
QY 61 FVQYKIMFSCSMKSSHQKPSGCWHISCNFPGCRTLAKYQGRQWKNEKDCWGTQELSCDL 120
Db 61 FVQYKI-----YGRQWKNEKDCWGTQELSCDL 88
QY 121 TSETSDIQBPYGRVRAASAGSYSEWSMTPRFTPPWNETKIDPPVMNITQVNGSLVILHA 180
Db 89 TSETSDIQBPYGRVRAASAGSYSEWSMTPRFTPPWNETKIDPPVMNITQVNGSLVILHA 148
QY 181 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 240
Db 149 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 208
QY 241 ABIYQPMLEDRRSQSRSEECVEIP 263
Db 209 ABIYQPMLEDRRSQSRSEECVEIP 231

RESULT 11
US-10-242-574-114
; Sequence 114, Application US/10242574
; Publication No. US20030138899A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C20
; CURRENT APPLICATION NUMBER: US/10/242,574
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
```

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; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 114
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-242-574-114

Query Match      85.1%; Score 1218; DB 12; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPMKHCFLGLISFFLTGVAGTQSTHESLKPQVQFSRNFHNILOQPGRALTGSSVY 60
Db 1 MPMKHCFLGLISFFLTGVAGTQSTHESLKPQVQFSRNFHNILOQPGRALTGSSVY 60
QY 61 FVOYKIMFSCSMKSSHQKPGCGWQHISCNFPFGCRTLAKYGORQWKNCDCWGTOELSCDL 120
Db 61 FVOYKI-----YQORQWKNCDCWGTOELSCDL 88
QY 121 TSSTSDIQEPYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVLILHA 180
Db 89 TSSTSDIQEPYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVLILHA 148
QY 181 PNLPRYQKEKNVSIEDYELLRYRFFIINNSLEKQKVEGAHRAVEIEALTPHSSYCVV 240
Db 149 PNLPRYQKEKNVSIEDYELLRYRFFIINNSLEKQKVEGAHRAVEIEALTPHSSYCVV 208
QY 241 AEIYQMLDRRSORSEERCVEIP 263
Db 209 AEIYQMLDRRSORSEERCVEIP 231
```

RESULT 12

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US-10-243-261-114
; Sequence 114, Application US/10243261
; Publication No. US20030138900A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C56
; CURRENT APPLICATION NUMBER: US/10/243,261
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
```

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; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 114
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-261-114

Query Match      85.1%; Score 1218; DB 12; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPMKHCFLGLISFFLTGVAGTQSTHESLKPQVQFSRNFHNILOQPGRALTGSSVY 60
Db 1 MPMKHCFLGLISFFLTGVAGTQSTHESLKPQVQFSRNFHNILOQPGRALTGSSVY 60
QY 61 FVOYKIMFSCSMKSSHQKPGCGWQHISCNFPFGCRTLAKYGORQWKNCDCWGTOELSCDL 120
Db 61 FVOYKI-----YQORQWKNCDCWGTOELSCDL 88
QY 121 TSSTSDIQEPYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVLILHA 180
Db 89 TSSTSDIQEPYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVLILHA 148
QY 181 PNLPRYQKEKNVSIEDYELLRYRFFIINNSLEKQKVEGAHRAVEIEALTPHSSYCVV 240
Db 149 PNLPRYQKEKNVSIEDYELLRYRFFIINNSLEKQKVEGAHRAVEIEALTPHSSYCVV 208
QY 241 AEIYQMLDRRSORSEERCVEIP 263
Db 209 AEIYQMLDRRSORSEERCVEIP 231
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RESULT 13

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US-10-243-282-114
; Sequence 114, Application US/10243282
; Publication No. US20030138901A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C50
; CURRENT APPLICATION NUMBER: US/10/243,282
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
```

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; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 114
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-282-114

Query Match      85.1%; Score 1218; DB 12; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MNPKECFGLFLISFFLTGAGTQSTHESLKPVQVQSRNFHNILOWQGRALTGNSVY 60
DB 1 MNPKECFGLFLISFFLTGAGTQSTHESLKPVQVQSRNFHNILOWQGRALTGNSVY 60
QY 61 FVOYKIMFSCSMKSHQKPGCGWHISCNPPGCRTLAKYQGRQWKNKEDCWGTQELSDDL 120
DB 61 FVOYKI-----YGRQWKNKEDCWGTQELSDDL 88
QY 121 TSETSDIOEPPYGRVRAASAGSYSEWSMTPTPTWMTETKIDPPVMNITQVNGSLVLHA 180
DB 89 TSETSDIOEPPYGRVRAASAGSYSEWSMTPTPTWMTETKIDPPVMNITQVNGSLVLHA 148
QY 181 PNLPRYQKKNVSDIYELLYRVFIINNSLEKQKVEGAHRAVEIEALTPHSSYCV 240
DB 149 PNLPRYQKKNVSDIYELLYRVFIINNSLEKQKVEGAHRAVEIEALTPHSSYCV 208
QY 241 AEIYQMLDRRSORSEERCV 263
DB 209 AEIYQMLDRRSORSEERCV 231

RESULT 14
US-10-243-402-114
; Sequence 114, Application US/10243402
; Publication No. US20030138902A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C39
; CURRENT APPLICATION NUMBER: US/10/243, 402
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27

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; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 114
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-402-114

Query Match      85.1%; Score 1218; DB 12; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MNPKECFGLFLISFFLTGAGTQSTHESLKPVQVQSRNFHNILOWQGRALTGNSVY 60
DB 1 MNPKECFGLFLISFFLTGAGTQSTHESLKPVQVQSRNFHNILOWQGRALTGNSVY 60
QY 61 FVOYKIMFSCSMKSHQKPGCGWHISCNPPGCRTLAKYQGRQWKNKEDCWGTQELSDDL 120
DB 61 FVOYKI-----YGRQWKNKEDCWGTQELSDDL 88
QY 121 TSETSDIOEPPYGRVRAASAGSYSEWSMTPTPTWMTETKIDPPVMNITQVNGSLVLHA 180
DB 89 TSETSDIOEPPYGRVRAASAGSYSEWSMTPTPTWMTETKIDPPVMNITQVNGSLVLHA 148
QY 181 PNLPRYQKKNVSDIYELLYRVFIINNSLEKQKVEGAHRAVEIEALTPHSSYCV 240
DB 149 PNLPRYQKKNVSDIYELLYRVFIINNSLEKQKVEGAHRAVEIEALTPHSSYCV 208
QY 241 AEIYQMLDRRSORSEERCV 263
DB 209 AEIYQMLDRRSORSEERCV 231

RESULT 15
US-10-243-431-114
; Sequence 114, Application US/10243431
; Publication No. US20030138903A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C37
; CURRENT APPLICATION NUMBER: US/10/243, 431
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10

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; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 114
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-431-114

Query Match      85.1%; Score 1218; DB 12; Length 231;
Best Local Similarity 87.8%; Pred. No. 2.6e-116;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Qy      1 MNPXKCFGLISFLTGAGTQTHESLKPRVQFQSRNFHNILOWQPGRALTGNSVY 60
Db      1 MNPXKCFGLISFLTGAGTQTHESLKPRVQFQSRNFHNILOWQPGRALTGNSVY 60

Qy      61 FVQYKIMFSCMKSSHQKPSGCWQHISCNPFPGCRTLAKYGORQWKNEKDCWGTQELSCDL 120
Db      61 FVQYKI-----YQQRQWKNEKDCWGTQELSCDL 88

Qy      121 TSETSDIQEPYIGRVRAASAGSYSEWSMTPTFTPWETKIDPPVMNITQVNGSLVILHA 180
Db      89 TSETSDIQEPYIGRVRAASAGSYSEWSMTPTFTPWETKIDPPVMNITQVNGSLVILHA 148

Qy      181 PNLPRYQKEKNVSIEDYELLVYRVIINNSLEKEQKYEGAHRAVEIALTPHSSYCVV 240
Db      149 PNLPRYQKEKNVSIEDYELLVYRVIINNSLEKEQKYEGAHRAVEIALTPHSSYCVV 208

Qy      241 AEIYQPMLDRRSRSEERCVEIP 263
Db      209 AEIYQPMLDRRSRSEERCVEIP 231
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Search completed: December 12, 2003, 12:24:05
Job time : 49.1424 secs


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SQ SEQUENCE 263 AA; 30550 MW; C36EBCESD78AC79B CRC64;
Query Match 100.0%; Score 1432; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.7e-131;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPPKHCFLGLISFLTLGVAGTQSTHESLKPRQVQFQSRNFHNLQWPGRALTGNSVY 60
Db 1 MPPKHCFLGLISFLTLGVAGTQSTHESLKPRQVQFQSRNFHNLQWPGRALTGNSVY 60

Qy 61 FVQYKIMFSCMSKSHQKPSGCWQHISCNPPGCRTLAKYQQRQWKNKDCWGTQELSCDL 120
Db 61 FVQYKIMFSCMSKSHQKPSGCWQHISCNPPGCRTLAKYQQRQWKNKDCWGTQELSCDL 120

Qy 121 TSETSDIQEYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVILHA 180
Db 121 TSETSDIQEYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVILHA 180

Qy 181 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQVYEGAHRAVEIALTPHSSYCVV 240
Db 181 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQVYEGAHRAVEIALTPHSSYCVV 240

Qy 241 AEIYQPMLDRRSQRSEERCVEIP 263
Db 241 AEIYQPMLDRRSQRSEERCVEIP 263

RESULT 2
Q96A41 PRELIMINARY; PRT; 231 AA.
AC Q96A41;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Soluble cytokine class II receptor, short isoform precursor
DE (Interleukin 22-binding protein CRF2-10) (Class II cytokine receptor)
DE (Interleukin-22 binding protein)
GN CRF2-S1 OR IL22BP OR IL22RA2 OR IL-22BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=21518574; PubMed=11607789;
RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S.,
RA Wolk K., Asadullah K., Sabat R.;
RT "A novel, soluble homologue of the human IL-10 receptor with
RT preferential expression in placenta.";
RL Genes Immun. 2:329-334 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286453; PubMed=11390454;
RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
RA Dickensheets H., Donnelly R.P., Pestka S.;
RT "Identification, cloning, and characterization of a novel soluble
RT receptor that binds IL-22 and neutralizes its activity.";
RL J. Immunol. 166:7096-7103 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396522; PubMed=11481447;
RA Xu W., Pressnell S.R., Parrish-Novak J., Kindsvogel W., Jaspers S.,
RA Chen Z., Dillon S.R., Gao Z., Gilbert T., Madden K., Schlutemeyer S.,
RA Yao L., Whitmore T.E., Chandrasekhar Y., Grant F.J., Maurer M.,
RA Jalinek L., Storey H.C., Brender T., Hammond A., Topouzis S.,
RA Clegg C.H., Foster D.C.;
RT "A soluble class II cytokine receptor, IL-22RA2, is a naturally
RT occurring IL-22 antagonist.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9511-9516 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;

RA Dumoutier L., Lejeune D., Renaud J.C.;
RT "Cloning and characterization of Interleukin-22 Binding Protein (IL-
RT 22BP), a natural antagonist of IL-TIF/IL-22.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ313161; CAC85634.1; -
DR EMBL; AY040566; AAK85714.1; -
DR EMBL; AY044429; AAK91775.1; -
DR EMBL; AJ297262; CAC83097.1; -
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 231 SOLUBLE CYTOKINE CLASS II RECEPTOR, SHORT
FT ISOFORM.
SQ SEQUENCE 231 AA; 26979 MW; 24A6912BFF75100F CRC64;
Query Match 85.1%; Score 1218; DB 4; Length 231;
Best Local Similarity 87.8%; Pred. No. 1.1e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Qy 1 MPPKHCFLGLISFLTLGVAGTQSTHESLKPRQVQFQSRNFHNLQWPGRALTGNSVY 60
Db 1 MPPKHCFLGLISFLTLGVAGTQSTHESLKPRQVQFQSRNFHNLQWPGRALTGNSVY 60

Qy 61 FVQYKIMFSCMSKSHQKPSGCWQHISCNPPGCRTLAKYQQRQWKNKDCWGTQELSCDL 120
Db 61 FVQYKI-----YQQRQWKNKDCWGTQELSCDL 88

Qy 121 TSETSDIQEYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVILHA 180
Db 89 TSETSDIQEYGRVRAASAGSYSEWSMTPTFTPMWETKIDPPVMNITQVNGSLVILHA 148

Qy 181 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQVYEGAHRAVEIALTPHSSYCVV 240
Db 149 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQVYEGAHRAVEIALTPHSSYCVV 208

Qy 241 AEIYQPMLDRRSQRSEERCVEIP 263
Db 209 AEIYQPMLDRRSQRSEERCVEIP 231

RESULT 3
Q96QRO PRELIMINARY; PRT; 130 AA.
AC Q96QRO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin 22-binding protein CRF2-10S.
GN IL22BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21286453; PubMed=11390454;
RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E.,
RA Dickensheets H., Donnelly R.P., Pestka S.;
RT "Identification, cloning, and characterization of a novel soluble
RT receptor that binds IL-22 and neutralizes its activity.";
RL J. Immunol. 166:7096-7103 (2001).
DR EMBL; AY040568; AAK85716.1; -
DR InterPro; IPR000282; Cytok_receptor_2.
SQ SEQUENCE 130 AA; 15128 MW; A165814C641F5B5B CRC64;
Query Match 46.7%; Score 669; DB 4; Length 130;
Best Local Similarity 79.8%; Pred. No. 2e-57;
Matches 125; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Qy 1 MPPKHCFLGLISFLTLGVAGTQSTHESLKPRQVQFQSRNFHNLQWPGRALTGNSVY 60
Db 1 MPPKHCFLGLISFLTLGVAGTQSTHESLKPRQVQFQSRNFHNLQWPGRALTGNSVY 60

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QY 61 FVQYKIMFSCMKSSHOKFSGCQWQHISCNFPFGCRTLAKYQORQWKNEKDCWGTQELSCDL 120
Db |||||
QY 61 FVQYKI-----YQORQWKNEKDCWGTQELSCDL 88
Db |||||

QY 121 TSETSDIQPYGRVRAAAGSYSEWSMTRPTPWME 157
Db |||||
QY 89 TSETSDIQPYGRVRAAAGSYSEWSMTRPTPWME 125
Db |||||

RESULT 4
Q9UHF4 PRELIMINARY; PRT; 553 AA.
AC Q9UHF4;
ID Q9UHF4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Class II cytokine receptor ZCYTOR7.
GN ZCYTOR7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Kho C., Jelmsberg A., Adams R., Whitmore T., Farrah T.,
RA O'Hara P.;
RT "Homo sapiens cytokine receptor homolog.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Prenell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184971; AAF01320.1; -.
DR HSP; P13726; 2HFT.
DR Gensu; HGNC:6003; IL20RA.
DR InterPro; IPR00282; Cytok receptor 2.
DR InterPro; IPR001187; Tissue_factor_.
DR Pfam; PF01108; Tissue_fac; 1.
KW Receptor.
SQ SEQUENCE 553 AA; 62533 MW; 7C23C8543B114659 CRC64;

Query Match 21.6%; Score 310; DB 4; Length 553;
Best Local Similarity 32.0%; Pred. No. 1.3e-21;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 30 KQORVQFOSRNFHNIQWPGRALTGNSSVYFVQYKIMFSCMKSSHOKFSGCQWQHISCN 89
Db |||||
QY 39 KPNITFLSINMKNVLTWTPPEGLOGVKVYTVQYFI----- 75
Db |||||
QY 90 FPGCRTLAKYQORQWKNEKDCWGTQELSCDLTSETSDIQEYPYGRVRAAAGSYSEWSMT 149
Db |||||
QY 76 -----YQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIGWTKCSKWAES 126
Db |||||
QY 150 PRFTPWETKIDPPVMNITQVNGSLVLHAPNLPRYQKEKNVSIEDYY-ELLRYVFII 208
Db |||||
QY 127 GRFPFLEQTQIGPPEVALTDEKISVVLTAPEKWRNPEDLPVSMQQTYSNLKYNVSL 186
Db |||||
QY 209 NNSLEKQKVEGAHRAVEIEALTPHSSVCVVAETIQPMLDRRSORSEERC 259
Db |||||
QY 187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVGPFPRAQPSKQC 236
Db |||||

RESULT 6
Q8BW64 PRELIMINARY; PRT; 546 AA.
AC Q8BW64;
ID Q8BW64;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Similar to BA204P2.1.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK054215; BAC35695.1; -.
SQ SEQUENCE 546 AA; 61978 MW; E7EC07DA3D49AF7F CRC64;

Query Match 19.3%; Score 276; DB 11; Length 546;
Best Local Similarity 28.6%; Pred. No. 2.6e-18;
Matches 67; Conservative 35; Mismatches 94; Indels 38; Gaps 4;

QY 30 KQORVQFOSRNFHNIQWPGRALTGNSSVYFVQYKIMFSCMKSSHOKFSGCQWQHISCN 89
Db |||||
QY 42 KPNITFLSINMKNVLTWTPPEGLOGVKVYTVQYFI----- 78
Db |||||
QY 90 FPGCRTLAKYQORQWKNEKDCWGTQELSCDLTSETSDIQEYPYGRVRAAAGSYSEWSMT 149
Db |||||
QY 79 -----YQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIGWTKCSKWAES 129
Db |||||
QY 150 PRFTPWETKIDPPVMNITQVNGSLVLHAPNLPRYQKEKNVSIEDYY-ELLRYVFII 208
Db |||||

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QY 61 FVQYKIMFSCMKSSHOKFSGCQWQHISCNFPFGCRTLAKYQORQWKNEKDCWGTQELSCDL 120
Db |||||
QY 61 FVQYKI-----YQORQWKNEKDCWGTQELSCDL 88
Db |||||

QY 121 TSETSDIQPYGRVRAAAGSYSEWSMTRPTPWME 157
Db |||||
QY 89 TSETSDIQPYGRVRAAAGSYSEWSMTRPTPWME 125
Db |||||

RESULT 4
Q9UHF4 PRELIMINARY; PRT; 553 AA.
AC Q9UHF4;
ID Q9UHF4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Class II cytokine receptor ZCYTOR7.
GN ZCYTOR7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Kho C., Jelmsberg A., Adams R., Whitmore T., Farrah T.,
RA O'Hara P.;
RT "Homo sapiens cytokine receptor homolog.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Prenell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184971; AAF01320.1; -.
DR HSP; P13726; 2HFT.
DR Gensu; HGNC:6003; IL20RA.
DR InterPro; IPR00282; Cytok receptor 2.
DR InterPro; IPR001187; Tissue_factor_.
DR Pfam; PF01108; Tissue_fac; 1.
KW Receptor.
SQ SEQUENCE 553 AA; 62533 MW; 7C23C8543B114659 CRC64;

Query Match 21.6%; Score 310; DB 4; Length 553;
Best Local Similarity 32.0%; Pred. No. 1.3e-21;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 30 KQORVQFOSRNFHNIQWPGRALTGNSSVYFVQYKIMFSCMKSSHOKFSGCQWQHISCN 89
Db |||||
QY 39 KPNITFLSINMKNVLTWTPPEGLOGVKVYTVQYFI----- 75
Db |||||
QY 90 FPGCRTLAKYQORQWKNEKDCWGTQELSCDLTSETSDIQEYPYGRVRAAAGSYSEWSMT 149
Db |||||
QY 76 -----YQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIGWTKCSKWAES 126
Db |||||
QY 150 PRFTPWETKIDPPVMNITQVNGSLVLHAPNLPRYQKEKNVSIEDYY-ELLRYVFII 208
Db |||||
QY 127 GRFPFLEQTQIGPPEVALTDEKISVVLTAPEKWRNPEDLPVSMQQTYSNLKYNVSL 186
Db |||||
QY 209 NNSLEKQKVEGAHRAVEIEALTPHSSVCVVAETIQPMLDRRSORSEERC 259
Db |||||
QY 187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVGPFPRAQPSKQC 236
Db |||||

RESULT 5
Q96SH8 PRELIMINARY; PRT; 553 AA.
AC Q96SH8;
ID Q96SH8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE BA204P2.1.1 (Interleukin 20 receptor alpha, isoform 1).
GN IL20RA.
OS Homo sapiens (Human).

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Db 130 ERFYPLETOVSPEVALTGTGKSIISIALTAPEKWKRNPODHTVSMQIYNLKNVSVY 189
QY 209 NNSLEKEQKVEG--AHRAVEIEALTPHSSYCVVAEIQPMLDRRSGEERCY 260
Db 190 NT---KSRRWOCVTNLTSLVLSWLEPNTLYCVHVESLVEGPPRLPMPQKCI 240
RESULT 7
Q96SH7 PRELIMINARY; PRT; 209 AA;
AC Q96SH7;
DT 01-DSC-2001 (TrEMBLrel. 19, Created)
DT 01-DSC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE BA204P2.1.3 (Interleukin 20 receptor alpha, isoform 3).
GN IL20RA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Griffiths C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL135902; CAC38376.1; -.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor.
SQ SEQUENCE 209 AA; 23616 MW; 467AB77BE3840361 CRC64;
Query Match 18.3%; Score 262; DB 4; Length 209;
Best Local Similarity 31.1%; Pred. No. 1.8e-17;
Matches 61; Conservative 29; Mismatches 72; Indels 34; Gaps 3;
QY 30 KPORVOFSRNFNIIQWPGRALTGNSSVYFVQYKIMFSCSMKSHQKPCGWQHSN 89
Db 39 KPNATIFLSINMKVNLQWTPPEGLQGVKTYTYQYFI----- 75
QY 90 FPGCRTLAKYQORWKNKEDCWGTQELSCDLTSETSDIOEPYGRVRAASAGSYSEWSMT 149
Db 76 -----YGQKWLKSECRNINRYCDLSAETSDYEHQYAKVKAIVGTCKSWAES 126
QY 150 PRFTPMWETKIDPPVNNITQVNGSLVILHAPNLPYRQKKNVSIEDYY-ELLYRVFII 208
Db 127 GRFYPLETQIGPPEVALITDEKSIWLTAPKWKRNPEDLFVSMQIYNLKNVSVL 186
QY 209 NNSLEKEQV-YEGAH 223
Db 187 NTKSNRTVSLKWNAGY 202
RESULT 8
Q9N6P7 PRELIMINARY; PRT; 574 AA.
AC Q9N6P7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Interleukin 22 receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal cortex;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029273; AAH29273.1; -.
DR Genew; HGNC:13700; IL22RA1.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor.
SQ SEQUENCE 574 AA; 63076 MW; D46CC71D496F3420 CRC64;
Query Match 16.8%; Score 240; DB 4; Length 574;
Best Local Similarity 28.6%; Pred. No. 8.9e-15;
Matches 69; Conservative 31; Mismatches 93; Indels 48; Gaps 6;
QY 21 GTQSTHESLKP---QRVQFSRNFNIIQWPGRALTGNSSVYFVQYKIMFSCSMKSH 76
Db 11 GSLAAHAPEDPSDLLQHVKFSQSNFENILTWDSGPEGTPD-TVYSIEYK----- 58
QY 77 QKPSGCWQHISCNFGPCRTLAKYQORWKNKEDCWGTQELSCDLTSETSDIOEPYGRVR 136
Db 59 -----TYGERDVAWKGCCQIRTRKSCNLTETGNLTLYYARVT 97
QY 137 AASAGSYSEWSMTPRFTPMWETKIDPPVNNITQVNGSLVILHAPNLPYRQKKNVSI 196
Db 98 AVSAGRSATKMTDRFSSLOHTTLKPPDVTCTSKVRSIQMIVHPTPTPIRAGDGHRLTLE 157
QY 197 D-YVELLYRVFIIINNSLEKEQKVE-----GAHRAVEIEALTPHSSYCVVAEIQPMLDR 251
Db 158 DIFHDLFVHLELVN-----RTYQMLGKGQREYEFFGLTPDTEFLGTIMICVPTWAKE 211
QY 252 S 252
Db 212 S 212
RESULT 9
Q9HB22 PRELIMINARY; PRT; 574 AA.
AC Q9HB22;
DT 01-NAR-2001 (TrEMBLrel. 16, Created)
DT 01-NAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
DE IL-22 receptor.
GN IL22R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469498; PubMed=10875937;
RA Xie M.H., Aggarwal S., Ho W.H., Foster J., Zhang Z., Stinson J.,
RA Wood W.I., Goddard A.D., Gurney A.L.;
RT "Interleukin (IL)-22, a Novel Human Cytokine That Signals through the
RT Interferon Receptor-related Proteins CRP2-4 and IL-22R.";
RL J. Biol. Chem. 275:31335-31339(2000).
DR EMBL; AF286095; AAG22073.1; -.
DR HSSP; P13726; 1TFH.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor.
SQ SEQUENCE 574 AA; 62977 MW; C179C7085C6F3420 CRC64;
Query Match 16.8%; Score 240; DB 4; Length 574;
Best Local Similarity 28.6%; Pred. No. 8.9e-15;
Matches 69; Conservative 31; Mismatches 93; Indels 48; Gaps 6;
QY 21 GTQSTHESLKP---QRVQFSRNFNIIQWPGRALTGNSSVYFVQYKIMFSCSMKSH 76
Db 11 GSLAAHAPEDPSDLLQHVKFSQSNFENILTWDSGPEGTPD-TVYSIEYK----- 58
QY 77 QKPSGCWQHISCNFGPCRTLAKYQORWKNKEDCWGTQELSCDLTSETSDIOEPYGRVR 136
Db 59 -----TYGERDVAWKGCCQIRTRKSCNLTETGNLTLYYARVT 97
QY 137 AASAGSYSEWSMTPRFTPMWETKIDPPVNNITQVNGSLVILHAPNLPYRQKKNVSI 196
Db 98 AVSAGRSATKMTDRFSSLOHTTLKPPDVTCTSKVRSIQMIVHPTPTPIRAGDGHRLTLE 157
QY 197 D-YVELLYRVFIIINNSLEKEQKVE-----GAHRAVEIEALTPHSSYCVVAEIQPMLDR 251
Db 158 DIFHDLFVHLELVN-----RTYQMLGKGQREYEFFGLTPDTEFLGTIMICVPTWAKE 211
QY 252 S 252
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Db 212 s 212
RESULT 10
Q99ND6 PRELIMINARY; PRT; 569 AA.
AC Q99ND6
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Interleukin-10 receptor, alpha chain precursor.
GN IL-10RA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Periphereal blood;
RA Ward H., Vignes S., Poole S., Bristow A.F.;
RT "The rat interleukin-10 receptor: cloning and sequencing of cDNA
RT coding for the alpha-chain protein sequence, and demonstration by
RT Western blotting of expression in rat brain.";
RL Cytokine 0:0-0(0).
DR EMBL; AJ305049; CAC24567.1; -.
DR InterPro; IPR000282; Cytok_receptor_2.
KW Receptor; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 569 INTERLEUKIN-10 RECEPTOR.
SQ SEQUENCE 569 AA; 63526 MW; 2354FD61DB351BD2 CRC64;

Query Match 13.4%; Score 192.5; DB 11; Length 569;
Best Local Similarity 25.2%; Pred. No. 3.8e-10;
Matches 72; Conservative 37; Mismatches 94; Indels 83; Gaps 13;

QY 1 MNPKHCFGLFLISFLTGTAGVAGTOSTHESLKQVQFQSRNFHNIQWQ--PGRALGNSS 58
Db 1 MLPR--LLPFLVSISSLSLGFRAHGTLPSPSSWFEARFFQHLRWMSIPNQ----SES 54
QY 59 VTFVQKIMFSCMSKSHQKPCSCWOHISCNFPGCRTLAKYQORQWKNKEDCWGTQELSC 118
Db 55 TY---YEV-----ALAKYGTGSIWKDIHICSKAQTLSC 83
QY 119 DLTSETSDI--QEPYVGRVRAASAGSYSEWSMT--PRFTPWETKIDPPVWNITQV----- 170
Db 84 DLTSTLDLYHSSGYRVRADVNSQYSNWTITETFT-----VDEVILTVDSTVTKVS 137
QY 171 NGSLVILHAPNLPYRYQKEKNVSIEDYYE-----LLYRVFT-----INNSLEKEQ 216
Db 138 NGFIYGTIHPP-----RPNLVPVGDVEYEQIFTHRIYRVCIKFSQKNITKIQEEN 190
QY 217 KYVEGAHRAVEIEALTPHSSYCVVAEIIYQPMLDRRSQRSEECVEI 262
Db 191 FTLEVPKRM-----RKFCVKWMPHVESRINKAEWSEEQCLHV 227

RESULT 11
Q9YGC8
ID Q9YGC8 PRELIMINARY; PRT; 341 AA.
AC Q9YGC8
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Interleukin-10 receptor 2.
GN IL10R2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RL receptor gene cluster";
RL Genome Res. 0:0-0(1999).
DR EMBL; AF082667; AADI3678.1; -.
DR EMBL; AF082666; AADI3671.1; -.
DR HSSP; P13726; 1AHW.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR001187; Tissue_factor.
DR Pfam; PF01108; Tissue_fac; 1.
DR PRINTS; PR00346; TISSUEFACTOR.
DR SMART; SM00060; FN3; 2.
KW Receptor.
SQ SEQUENCE 341 AA; 39062 MW; 18027239BF8A9C87 CRC64;

Query Match 12.6%; Score 180.5; DB 13; Length 341;
Best Local Similarity 24.2%; Pred. No. 3e-09;
Matches 56; Conservative 37; Mismatches 97; Indels 41; Gaps 7;

QY 30 KPOVQFQSRNFHNIQWOPGRALTCNSSVYFYQYKIMFSCMSKSHQKPCSCWOHISCN 89
Db 23 KPNARISSVNFPSVLLMDPPGVKGNLS-YTVQAKSIF-----PKQNFNNVTIN 71
QY 90 FPGCRTLAKYQORQWKNKEDCWGTQELSCDLTSETSDIQEPYVGRVRAASAGSYSEWSMT 149
Db 72 L-----NVECDVSS--LSVYGAVLVIRVTEWEDHSDWAVV 106
QY 150 PRFTPWETKIDPPVWNITQVNGSLVILHAPNLPYRYQKEKNVSIEDYY-ELLYRVFTII 208
Db 107 -RFKPMADTVIGPPSVNKSSEGLTHVDTGPAADREHDK---WSLKQYVGSWIRLYW 162
QY 209 NNSLEKEQVYEGAHRAVEIEALTPHSSYCVVAEIIYQPMLDRRSQRSEERC 259
Db 163 KKGSKNKKVIHIDTKHNSILSQLEPWTIYCIQVGVIPENWNTGERSQELC 213

RESULT 12
Q90W13
ID Q90W13 PRELIMINARY; PRT; 294 AA.
AC Q90W13
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Tissue factor precursor.
GN TF.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RA Sangrador-Vegas A., Smith T.J.;
RT "Molecular cloning of rainbow trout (Oncorhynchus mykiss) tissue factor
RT precursor by use of suppression subtractive hybridisation.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ295167; CAC82787.1; -.
DR InterPro; IPR000282; Cytok_receptor_2.
DR Pfam; PF01108; Tissue_fac; 1.
DR PRINTS; PR00346; TISSUEFACTOR.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 294 TISSUE FACTOR.
SQ SEQUENCE 294 AA; 33404 MW; 105DDDA107E54EDE CRC64;

Query Match 12.1%; Score 173.5; DB 13; Length 294;
Best Local Similarity 26.8%; Pred. No. 1.2e-08;
Matches 74; Conservative 34; Mismatches 91; Indels 77; Gaps 14;

QY 9 GFLIS--FFLTGACTQSTHESLKQVQFQSRNFHNIQWOPGRALTCNSSVYFYQYKI 66
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Db 11 GVLSSVLTGAAGEDYFPEAMD---VQWVSNNFKTILTWGP-----EFTNY--ITYV 59
Qy 67 MFSCSMKSHQKPGSCGWHISCNFPGCKTLAKYQORQWKNKEDCWGTQELSCDLTSETSD 126
Db 60 EFSRVGDKORQNP-----HCIRSRTECDLTNELRN 90
Qy 127 IQEPIYGRVRAASAGSYSE-----WSMTPRFTPWETKIDPPVNMNITQVNGS 173
Db 91 LQETV-----SADILSEPLPGVTSDLVEFPYTRAERFSYKTKIGCPAFKIVQSDK 143
Qy 174 LLVLHAPN-LPYRYQKEKNVSIEDY--ELLYRVFIIN--NSLEKEQVYEGAHRAVEI 228
Db 144 TKMTLHIQDPLTPLYKDBOLLTIRDFKSLKRV-IVNKAGSTGKKEKMSD--LRDEL 200
Qy 229 EALTPHSSYCVVAEIQMLDRRSOR-----SEERC 259
Db 201 TNLDKGOSYCVIVAAYIP--SRSAQKRLGDWSKAQC 234

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RESULT 13

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Qy IHWO Q9YHWO PRELIMINARY; PRT; 569 AA.
AC Q9YHWO;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Interferon alpha/beta receptor 1.
GN IFNARI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99177346; PubMed=10077530;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the Interferon/Interleukin-10
RT receptor gene cluster.";
RL Genome Res. 9:242-250(1999).
DR EMBL; AF082664; AAD13669.1; -.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR003961; FN_III.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 569 AA; 64055 MW; 6A757DDFB891B605 CRC64;

```

```

Query Match 10.9%; Score 155.5; DB 13; Length 569;
Best Local Similarity 23.2%; Pred. No. 1.5e-06;
Matches 63; Conservative 38; Mismatches 101; Indels 69; Gaps 12;

Qy 3 PKHCFGLISFFLTGVAGTOSTHSLKQVQFSRNFHNILOQWPGRALTGSSV-YF 61
Db 224 PIHC-----IKTKVNDLLCPTNVRVFLNMKFYLLWDNHY-----NEHVITYT 267
Qy 62 VQYKMFSCSMKSHQKPGSCGWHISCNFPGCKTLAKYQORQWKNKEDCWGTQELSCDLT 121
Db 268 VOYLTGY---LKNLYDDYSKKWKVS---GCENIT-----SMKCNLS 303
Qy 122 SETSDIQBPYGRVRAASAGSYSEWSMTPRFTPWETKIDPPVMN-----ITQVN 171
Db 304 SVIKPTSASYFRVQAMN--EYKSCLSK-----DVEVDPVTNEIGPPDVKVDISD-- 353
Qy 172 GSLVLHAPNLPYRYQKEKNVSIEDYELLYRVFIINSL--EKEQKYEGAHRAVEIE 229
Db 354 ----VLLHIKITPPGPGGNKIMS--DLYDFSQILYWKNSDNEBEVKMKETKQTATVS 407
Qy 230 ALTPHSSYCVVAEIQMLDRRSORSEERC 260
Db 408 DLAPSTLYCVKQAFSEAYNKSSDFSRECI 438

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RESULT 15

```

Qy IHWO Q8IV66 PRELIMINARY; PRT; 244 AA.
AC Q8IV66;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Soluble isoform of Likely interleukin or cytokine receptor 2.
GN LICR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dumoutier L., Renauld J.C.;
RT "Cloning and characterization of LICR-2, a new type 2 cytokine
RT receptor gene.";

```

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ534331; CAD58830.1; -.

SQ SEQUENCE 244 AA; 27536 MW; A6F3310C13FCC083 CRC64;

Query Match 10.5%; Score 151; DB 4; Length 244;

Query Match 10.5%; Score 151; DB 4; Length 244;
 Best Local Similarity 24.3%; Pred. No. 1.5e-06;
 Matches 63; Conservative 32; Mismatches 76; Indels 88; Gaps 13;

QY 31 PQRVQFSRNFHNILQWPGRALTGNSS--VFVQYKIMFSCSMKSSHQKPSGCWOHISC 88

[illegible]

Db 27 PQNVTLISQNFVSVYLTWLPG---LGNPQDVTFVAYQ-----SSPT-----64

89 NBPCCBET A VVCOBOLWAVTDCNCTCOTY CCRV BC

QY 89 NPPGCR TLAKY GQRQWK NKEDCWGTQELSCDLTS-ETSDIQEPYGRVRAASAGSYSEWS 147

Db 65 -----RRRRREVEECAGTKELLCSMMCIKKODI.YNKEGCVETVSPSSKSPW 112

DB -----RRRWREVEECAGTKELLCSMMCLKKQDLYNKFGRVRTVSPSSKSPWV 112

Qy 148 MTPRFTPWETKIDPPVMNITQVNGSLLVILHA-----PNLPYRYQKEKNVSIEDYYE 200

140 P I A T A L F W M E I K A D F F V M N I I Q V N G S L U V I T H R A -----P N L P R Y Q R K N V S I D Y Y E 200
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Db 113 ESEYDYLFEVEPAPVLVTQTE---EILSANATYQLPPCMP-----PLDLKVE 159

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QY 201 LLVRFIINSLKEQKVVEGAHRAVEIALTPHSS-----YCVVAE-IYQP 246

Dh

160 VAE-----WKECACNKT- Y BDTMBUCOCBICVCTMY CNA QNTTICR CCBCTVTYME CCA

Db 160 VAF-----WKEGAGNKT-LFPVTPHGQPVQITLQPAASEHHCLSLARTIYTF 204

QY 247 MLDPRSORSEERC--VEIP 263

247 MLDRKSRSEERC--VEIP 263

Dbb 205 SVPKYSKFSKPTCFLLVPP 223

Search completed: December 12, 2003, 12:27:20
Job time : 56.383 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2003, 12:15:52 ; Search time 66.8644 Seconds
(without alignments)
624.325 Million cell updates/sec

Title: US-10-047-264A-4

Perfect score: 1432

Sequence: 1 MPMKHCFLGLISFLITGVA.....YQPLDRSRSEERCVSEIP 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 1432 | 100.0 | 263 | ABJ10499 | Cytokine receptor |
| 2 | 1432 | 100.0 | 263 | AAE17321 | Human cytokine rec |
| 3 | 1428 | 99.7 | 263 | AAO17382 | Human cytokine rec |
| 4 | 1427 | 99.7 | 262 | AAU09186 | Human PRO19598 pol |
| 5 | 1397 | 97.6 | 263 | AAU080324 | Human IL-TIF/IL-22 |
| 6 | 1218 | 85.1 | 231 | AAE05048 | Human ZCYTO18 solu |
| 7 | 1218 | 85.1 | 231 | AAE02460 | Human DNAX cytokin |
| 8 | 1218 | 85.1 | 231 | AAE62657 | Human cytokine rec |
| 9 | 1218 | 85.1 | 231 | AAE28600 | Human Zcytor16 pro |

| | | | | | | |
|----|-------|------|-----|----|----------|--------------------|
| 10 | 1218 | 85.1 | 231 | 23 | ABJ10498 | Cytokine receptor |
| 11 | 1218 | 85.1 | 231 | 23 | AAO17381 | Human cytokine rec |
| 12 | 1218 | 85.1 | 231 | 23 | AAU08000 | Human IL-TIF/IL-22 |
| 13 | 1218 | 85.1 | 231 | 23 | ABG34086 | Human Pro peptide |
| 14 | 1218 | 85.1 | 231 | 23 | AAE17320 | Human cytokine rec |
| 15 | 1218 | 85.1 | 231 | 23 | AAE30826 | Human cytokine rec |
| 16 | 1218 | 85.1 | 231 | 24 | AAE30838 | Human cytokine rec |
| 17 | 1217 | 85.0 | 231 | 23 | ABJ10519 | Cytokine receptor |
| 18 | 1215 | 84.8 | 231 | 23 | ABJ10511 | Cytokine receptor |
| 19 | 1215 | 84.8 | 231 | 23 | ABJ10512 | Cytokine receptor |
| 20 | 1215 | 84.8 | 231 | 23 | ABJ10514 | Cytokine receptor |
| 21 | 1215 | 84.8 | 231 | 23 | ABJ10516 | Cytokine receptor |
| 22 | 1213 | 84.7 | 231 | 23 | ABJ10509 | Cytokine receptor |
| 23 | 1213 | 84.7 | 231 | 23 | ABJ10517 | Cytokine receptor |
| 24 | 1213 | 84.7 | 231 | 23 | ABJ10518 | Cytokine receptor |
| 25 | 1212 | 84.6 | 231 | 23 | ABJ10513 | Cytokine receptor |
| 26 | 1212 | 84.6 | 231 | 23 | ABJ10515 | Cytokine receptor |
| 27 | 1210 | 84.5 | 231 | 23 | ABJ10510 | Cytokine receptor |
| 28 | 1114 | 77.8 | 214 | 23 | AAE17319 | Human cytokine rec |
| 29 | 1104 | 77.1 | 210 | 22 | AAE62663 | Human zcytor16 ext |
| 30 | 1104 | 77.1 | 210 | 22 | AAE28607 | Human Zcytor16 pro |
| 31 | 1104 | 77.1 | 210 | 24 | AAE30832 | Human Zcytor16 ext |
| 32 | 1050 | 73.3 | 249 | 22 | AAE02458 | Human DNAX cytokin |
| 33 | 1050 | 73.3 | 249 | 22 | AAE02458 | Human cytokine rec |
| 34 | 802.5 | 56.0 | 230 | 23 | ABJ10501 | Cytokine receptor |
| 35 | 800.5 | 55.9 | 230 | 23 | AAE28616 | Cytokine receptor |
| 36 | 792.5 | 55.3 | 230 | 23 | AAE28613 | Mouse Zcytor16 pro |
| 37 | 669 | 46.7 | 130 | 23 | ABJ10500 | Mouse Zcytor16 pro |
| 38 | 661 | 46.2 | 130 | 22 | AAE02461 | Cytokine receptor |
| 39 | 310 | 21.6 | 207 | 22 | AAE85289 | Human DNAX cytokin |
| 40 | 310 | 21.6 | 207 | 22 | ABG67220 | Human IL-20 recept |
| 41 | 310 | 21.6 | 214 | 22 | ABE85287 | Interleukin-20 sub |
| 42 | 310 | 21.6 | 214 | 22 | ABG67218 | Human IL-20 recept |
| 43 | 310 | 21.6 | 217 | 22 | AAE85280 | IL-20RA-Ig gammal |
| 44 | 310 | 21.6 | 217 | 22 | ABG67211 | Interleukin-20 sub |
| 45 | 310 | 21.6 | 221 | 22 | AAE85269 | Human IL-20 recept |

ALIGNMENTS

RESULT 1

ABJ10499

ID ABJ10499 standard; Protein; 263 AA.

XX ABJ10499;

AC ABJ10499;

XX 21-NOV-2002 (first entry)

DT Cytokine receptor family 2 (CRF2) related protein SEQ ID No 4.

DE Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW antinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;
KW gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;
KW interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW inflammation.

XX Unidentified.

XX WO200266647-A2.

PN 29-AUG-2002.

XX 14-JAN-2002; 2002WO-US00986.

XX 12-JAN-2001; 2001US-261442P.

PR 06-FEB-2001; 2001US-267021P.

PR 23-FEB-2001; 2001US-270835P.

XX (GEM) GENETICS INST LLC.

PA Fouser L, Liu W, Deng B;

PI

XX WPI: 2002-674946/72.
 DR N-PSDB; ABO8217.
 XX
 PT New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for
 PT diagnosing and treating disorders with abnormal CRF2-12 activity such
 PT as autoimmune diseases like rheumatoid arthritis, multiple sclerosis
 PT and inflammation -
 XX
 PS Claim 2; Page 7; 91pp; English.
 XX
 CC The invention relates to an isolated type 2 cytokine receptor family
 CC (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids
 CC 21-66 of a 231 residue amino acid sequence, given in the specification,
 CC or its complement. The compositions and methods of the present invention
 CC are useful for diagnosing, screening and treating disorders associated
 CC with abnormal CRF2-12 activity such as autoimmune diseases like
 CC rheumatoid arthritis, multiple sclerosis and inflammation. This sequence
 CC represents a cytokine receptor family 2 (CRF2-12) protein relating to the
 CC invention.
 XX
 SQ Sequence 263 AA;

Query Match 100.0%; Score 1432; DB 23; Length 263;
 Best Local Similarity 100.0%; Pred. No. 6.7e-135;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPXCFGLIFLISFLTGAGTQSTHESLKQPVQFQSRNFHILQWQGRALTGNSVY 60
 DB 1 MNPXCFGLIFLISFLTGAGTQSTHESLKQPVQFQSRNFHILQWQGRALTGNSVY 60
 QY 61 FVQYKIMFSCMSKSHQKPSGQWHSICNFPQCRITLAKYQGWKNKEDCWGTQSLCDL 120
 DB 61 FVQYKIMFSCMSKSHQKPSGQWHSICNFPQCRITLAKYQGWKNKEDCWGTQSLCDL 120
 QY 121 TSETSDIQEYGRVRAASAGSYSEMSMTPTPTWETKIDPPVNNITQVNGSLVLHA 180
 DB 121 TSETSDIQEYGRVRAASAGSYSEMSMTPTPTWETKIDPPVNNITQVNGSLVLHA 180
 QY 181 PNLPRYQKQKNSIEDYELLYRVIINNSLEKQKVEGAHRAVEALTPHSSYCVV 240
 DB 181 PNLPRYQKQKNSIEDYELLYRVIINNSLEKQKVEGAHRAVEALTPHSSYCVV 240
 QY 241 AEIYQPMIDRRSQSRSEERCEVP 263
 DB 241 AEIYQPMIDRRSQSRSEERCEVP 263

RESULT 2
 ID AAE17321 standard; Protein; 263 AA.
 XX
 AC AAE17321;
 XX
 DT 18-APR-2002 (first entry)
 XX
 DE Human cytokine receptor protein, sbg456548Cytora #3.
 XX
 KW Human; therapy; wound healing disorder; vaccine; cancer; infection;
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
 KW depression; cardiovascular disease; myocardial infarction; renal failure;
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
 KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;
 KW neutropenic; cirrhosis; Hodgkin's disease; antileptetic; antiinflammatory;
 KW haemostatic; vulnery; anticonvulsant; antirheumatic; neuroprotective;
 KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
 KW allergy; cytokine receptor.
 XX
 OS Homo sapiens.

XX WO200198342-A1.
 XX
 PD 27-DEC-2001.
 XX
 XX 22-JUN-2001; 2001WO-US19929.
 XX
 XX 22-JUN-2000; 2000US-213156P.
 XX
 XX 22-JUN-2000; 2000US-213161P.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
 XX Murdoch PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
 XX WPI; 2002-139783/18.
 XX N-PSDB; AAD27816.
 XX
 PT Novel secreted and membrane-associated polypeptides and polynucleotides
 PT useful for preventing, ameliorating or correcting dysfunction or
 PT disease including diabetes, cancer, hypertension and growth
 PT abnormalities -
 XX
 PS Claim 1; Page 133-134; 138pp; English.
 XX
 CC The invention relates to secreted and membrane-associated polypeptides
 CC and polynucleotides. The sequences of the invention are useful in
 CC diagnostic assays for detecting diseases associated with inappropriate
 CC activity or levels of these polynucleotides, and in identifying their
 CC agonists and antagonists that are potentially useful in therapy. The
 CC sequences of the invention are useful as vaccines for inducing
 CC immunological response. The sequences of the invention are useful for
 CC treating cancers, infections, autoimmune disorders, haematopoietic
 CC disorders, wound healing disorders, cholesterol ester storage disease,
 CC inflammation, congenital muscular dystrophy, junctional epidermolysis
 CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
 CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
 CC allergies, schizophrenia, sbg442445PROA-associated disorders,
 CC septicaemia, psoriasis, inflammatory bowel disease, transplant rejection,
 CC graft versus host disease, ischaemia, stroke, acute respiratory disease
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
 CC brain disorders including paraneuronal palsy, myotonic dystrophy,
 CC depression, anxiety disorders and sleep disorders, cardiovascular
 CC diseases including congestive heart failure and myocardial infarction,
 CC respiratory diseases including chronic obstructive pulmonary disease,
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders
 CC including hypercholesterolaemia, hypertiglyceridaemia, cirrhosis, viral
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
 CC and tendinitis, gastrointestinal diseases including intestinal
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
 CC reproductive diseases including low testosterone and male infertility.
 CC The present sequence is human cytokine receptor.
 XX
 SQ Sequence 263 AA;

Query Match 100.0%; Score 1432; DB 23; Length 263;
 Best Local Similarity 100.0%; Pred. No. 6.7e-135;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPXCFGLIFLISFLTGAGTQSTHESLKQPVQFQSRNFHILQWQGRALTGNSVY 60
 DB 1 MNPXCFGLIFLISFLTGAGTQSTHESLKQPVQFQSRNFHILQWQGRALTGNSVY 60
 QY 61 FVQYKIMFSCMSKSHQKPSGQWHSICNFPQCRITLAKYQGWKNKEDCWGTQSLCDL 120
 DB 61 FVQYKIMFSCMSKSHQKPSGQWHSICNFPQCRITLAKYQGWKNKEDCWGTQSLCDL 120
 QY 121 TSETSDIQEYGRVRAASAGSYSEMSMTPTPTWETKIDPPVNNITQVNGSLVLHA 180

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121 TSETSDIOEPYGRVRAASAGSYSEWSMTPRFTPWETKIDPPVMNITQVNGSLVILHA 180
181 PNLPRYQKEKNVSIEDYELLYRVFIIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 240
181 PNLPRYQKEKNVSIEDYELLYRVFIIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVV 240
241 AEIYQPMLEDRRSQSEERCEVEIP 263
241 AEIYQPMLEDRRSQSEERCEVEIP 263

RESULT 3
AAO17382
ID AAO17382 standard; Protein; 263 AA.
XX
AC AAO17382;
XX
DT 08-AUG-2002 (first entry)
XX
DE Human cytokine receptor variant 3.
XX
KW Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;
KW ulcerative colitis; transplant rejection; abortion; antipsoriatic;
KW immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antitumor; cytostatic; dermatological;
KW chromosome 6q24.1-25.2; receptor.
XX
OS Homo sapiens.
XX
PN EPI191035-A2.
XX
PD 27-MAR-2002.
XX
XX 24-AUG-2001; 2001EP-0250307.
XX
XX 25-SEP-2000; 2000DE-1048626.
XX
XX 17-NOV-2000; 2000DE-1058907.
XX
XX 19-DEC-2000; 2000DE-1064906.
XX
XX (SCHD ) SCHERING AG.
XX
XX Weiss B, Sabat R, Assadullah K, Toshi L;
XX
XX WPI; 2002-332210/37.
XX
XX N-PSDB; AAL46001.
XX
XX New nucleic acid encoding soluble cytokine receptor, useful for
XX diagnosis and treatment of e.g. immune disease, also related protein
XX and antibodies -
XX
XX Claim 6; Page 15; 21pp; German.
XX
XX The present invention provides the protein and coding sequences of 3
XX variants of a human cytokine receptor. The sequences can be used in the
XX diagnosis, prevention and treatment of immune diseases, including
XX psoriasis, cancer, chronic/life-threatening infections, rheumatoid
XX arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
XX transplant rejection and in reproductive medicine, e.g. for diagnosing
XX abnormal immune reactions which cause abortions. The present sequence is
XX variant 3 of the invention.
XX
XX Sequence 263 AA;
XX
XX Query Match 99.7%; Score 1428; DB 23; Length 263;
XX Best Local Similarity 99.6%; Pred. No. 1.7e-134;
XX Matches 262; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MPPKHCFLGLISFLTGACTQSTHESLKPQVQFSRNFHNIQWPGKALTGNSVY 60
XX 1 MPPKHCFLGLISFLTGACTQSTHESLKPQVQFSRNFHNIQWPGKALTGNSVY 60

```

(GETH) GENENTECH INC.

Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;

PI Tamas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-625876/72.
 DR N-PSDB; AAS15368.
 XX
 XX Nucleic acids encoding PRO polypeptides, useful for detecting and
 PT treating immune related diseases and disorders in mammals including
 PT autoimmune diseases, inflammatory diseases and asthma -
 XX
 XX Claim 10; Fig 18; 122pp; English.
 XX
 CC The present invention relates to the isolation of 9 novel human PRO
 CC polypeptides and the cDNA sequences (AAS15360-AAS15368) encoding them.
 CC The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444,
 CC PRO3151, PRO4322, PRO9964, PRO10008 and PRO19598. The cDNA sequences
 CC encoding these PRO polypeptides have been designated as clones
 CC DNA64886-1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273,
 CC DNA92223-2567, DNA96973, DNA101921 and DNA145887 respectively.
 CC Compositions (e.g. vaccines) containing PRO polypeptides and methods of
 CC using these compositions are useful in the treatment and diagnosis of
 CC immune-related disorders. Such disorders include immune-mediated
 CC inflammatory disorders (e.g. osteoarthritis), non-immune-mediated
 CC inflammatory disorders (e.g. diabetes mellitus), infectious disorders
 CC (e.g. granulomatous hepatitis), immunodeficiency disorders (e.g. AIDS),
 CC autoimmune disorders (e.g. rheumatoid arthritis), immune-related renal
 CC diseases (e.g. cirrhosis), demyelinating diseases of the peripheral or
 CC central nervous system (e.g. Guillain-Barre syndrome), immune-mediated
 CC skin diseases (e.g. contact dermatitis), neoplasias and transplantation
 CC associated diseases. The polynucleotide sequences of the invention may
 CC be used in gene therapy. AAU09178-AAU09186 represent the novel human
 CC PRO polypeptides of the invention.
 XX
 XX Sequence 262 AA;
 SQ
 Query Match 99.7%; Score 1427; DB 22; Length 262;
 Best Local Similarity 100.0%; Pred. No. 2.1e-134; Mismatches 0; Indels 0; Gaps 0;
 Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MPKCHFLGLISFFLTGVAGTQSTHESLKPQVQFQSRNFHNLQWQGRALTGNSVYF 61
 Db 1 MPKCHFLGLISFFLTGVAGTQSTHESLKPQVQFQSRNFHNLQWQGRALTGNSVYF 60
 QY 62 VOYKIMFSCSMKSHQKPSGCGWHISCNFPQGRITLAKYQORWKNKEDCWGTQELSCDLT 121
 Db 61 VOYKIMFSCSMKSHQKPSGCGWHISCNFPQGRITLAKYQORWKNKEDCWGTQELSCDLT 120
 QY 122 TSETSDIQEPYGRVRAASAGSYSEWSMTFRTPPWETKIDPPVNNITQVNGSLVILHAP 181
 Db 121 TSETSDIQEPYGRVRAASAGSYSEWSMTFRTPPWETKIDPPVNNITQVNGSLVILHAP 180
 QY 182 NLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVWA 241
 Db 181 NLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVWA 240
 QY 242 EIYQPMDDRQRSEERCVEIP 263
 Db 241 EIYQPMDDRQRSEERCVEIP 262
 RESULT 5
 AAU80324
 ID AAU80324 standard; Protein; 263 AA.
 XX
 AC AAU80324;
 XX
 XX 15-JUL-2002 (first entry)
 DT
 XX Human IL-TIF/IL-22 binding protein #2.
 DE
 XX Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
 KW IL-TIF/IL-22 antagonist.
 KW
 OS Homo sapiens.

XX WO200224912-A2.
 PN 28-MAR-2002.
 PD
 XX 21-SEP-2001; 2001WO-US2959576.
 PF
 XX 22-SEP-2000; 2000US-234583P.
 PR 03-NOV-2000; 2000US-245495P.
 PR 31-JUL-2001; 2001US-0919162.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Renaud J, Dumoutier L;
 PI WPI; 2002-383190/41.
 XX N-PSDB; ABK50080.
 DR
 XX Polynucleotide and polypeptide of soluble protein which binds to
 PT interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
 PT cell -
 XX
 XX Claim 14; Page 41-42; 42pp; English.
 XX
 CC The present invention relates to a new polynucleotide that encodes a
 CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
 CC to as IL-22BP), where the complementary sequence of the invention
 CC hybridises under stringent conditions to a nucleotide sequence of 2271
 CC or 2366 base pairs, as given in the specification. The molecules of the
 CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
 CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
 CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
 CC in vitro, and for obtaining an antibody molecule specific for the soluble
 CC binding protein of the invention, from a population or panel of antibody
 CC molecules of diverse binding specificity. The soluble protein is further
 CC useful in manufacture of a medicament for treating an IL-22 mediated
 CC disease and for assaying an agent, preferably an antibody or a peptide
 CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
 CC of the soluble protein to IL-TIF/IL-22, where the agent identified is
 CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
 CC disorder. The antibody is useful for determining presence of the soluble
 CC protein, where the antibody is detectably labelled. The present amino
 CC acid sequence represents the human IL-TIF/IL-22 binding protein #2 of
 CC the invention.
 XX
 XX Sequence 263 AA;
 SQ
 Query Match 97.6%; Score 1397; DB 23; Length 263;
 Best Local Similarity 98.1%; Pred. No. 2.1e-131;
 Matches 258; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MPMKCHFLGLISFFLTGVAGTQSTHESLKPQVQFQSRNFHNLQWQGRALTGNSVY 60
 Db 1 MPMKCHFLGLISFFLTGVAGTQSTHESLKPQVQFQSRNFHNLQWQGRALTGNSVY 60
 QY 61 FVOYKIMFSCSMKSHQKPSGCGWHISCNFPQGRITLAKYQORWKNKEDCWGTQELSCDL 120
 Db 61 FVOYKIMFSCSMKSHQKPSGCGWHISCNFPQGRITLAKYQORWKNKEDCWGTQELSCDL 120
 QY 121 TSETSDIQEPYGRVRAASAGSYSEWSMTFRTPPWETKIDPPVNNITQVNGSLVILHA 180
 Db 121 TSETSDIQEPYGRVRAASAGSYSEWSMTFRTPPWETKIDPPVNNITQVNGSLVILHA 180
 QY 181 PNLPYRQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVW 240
 Db 181 PNLPYRQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVW 240
 QY 241 AEIYQPMDDRQRSEERCVEIP 263
 Db 241 AEIYQPMDDRQRSEERCVEIP 263
 RESULT 6

| | |
|--|---|
| AAE05048 | AAE02460 |
| ID AAE05048 standard; Protein; 231 AA. | ID AAE02460 standard; Protein; 231 AA. |
| AC AAE05048; | AC AAE02460; |
| XX 10-SEP-2001 (first entry) | XX 10-AUG-2001 (first entry) |
| DT | DT |
| DE Human ZCYTO18 soluble receptor antagonist, zcytor16 protein. | DE Human DNAX cytokine receptor subunit 4.2 (DCRS4.2). |
| XX | XX |
| XX Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality; | XX Human; immunomodulator; DNAX cytokine receptor subunit 4.2; DCRS4.2; |
| KW cancer; inflammation; gene therapy; zcytor16. | KW therapy; immunological disorder; drug screening; cell development; |
| XX | XX |
| OS Homo sapiens. | OS Homo sapiens. |
| XX | XX |
| XX W0200146422-A1. | XX |
| XX | XX |
| PD 28-JUN-2001. | PD 25-MAY-2001. |
| XX | XX |
| XX 22-DEC-2000; 2000WO-US35308. | XX 16-NOV-2000; 2000WO-US31363. |
| XX | XX |
| XX 23-DEC-1999; 99US-0471767. | XX 18-NOV-1999; 99US-0443060. |
| PR | PR |
| PR 01-DEC-2000; 2000US-0250841. | PR 13-DEC-1999; 99US-0170320. |
| XX | XX |
| XX (ZYMO) ZYMOGENETICS INC. | XX (SCHE) SCHERING CORP. |
| XX | XX |
| XX Presnell SR, Kindsvogel W; | XX Gorman DM; |
| XX | XX |
| XX WPI; 2001-408648/43. | XX WPI; 2001-343800/36. |
| DR | DR |
| DR N-PSDB; AAD09745. | DR N-PSDB; AAD06414. |
| XX | XX |
| XX Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer - | XX New mammalian receptor proteins related to cytokine receptors, useful |
| XX | XX for regulating cell development and for diagnosis and treatment of |
| XX | XX immunological disorders - |
| PS Example 13A; Page 158-159; 167pp; English. | PS Claim 3; Page 23; 124pp; English. |
| XX | XX |
| XX The patent discloses novel human cytokine, ZCYTO18 protein and its | XX The present sequence is human DNAX cytokine receptor subunit 4.2 |
| CC corresponding DNA. ZCYTO18 protein induces proliferation of cells | CC (DCRS4.2). DCRS4 gene is located on chromosome 6q24.1-25.2. |
| CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity | CC Cytokine receptors, fragments and antibodies are useful for treating |
| CC in K5626 cells. ZCYTO18 DNA is useful for detecting a genetic | CC immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are |
| CC abnormality in a patient. ZCYTO18 DNA and its antibodies are useful | CC useful in drug screening to identify compounds having binding affinity |
| CC for detecting cancer and inflammation. ZCYTO18 protein is useful for | CC to the receptor subunit. Modulators of DCRS are useful for modulating |
| CC killing cancer cells. It is useful for increasing platelets in a | CC the physiology or development of a cell or tissue culture cells. A |
| CC patient or injured tissue. It is also used in gene therapy. | CC purified DCRS is useful as a reagent to detect antibodies generated in |
| CC The present sequence is human zcytor16, which is a naturally expressed | CC response to the presence of elevated levels of expression, or |
| CC soluble receptor antagonist of ZCYTO18 protein. | CC immunological disorders which lead to production of antibody to the |
| XX | XX endogenous receptor. Cytokine receptor sequences are useful as probes |
| XX | XX for detecting levels of the cytokine receptor in patients suspected of |
| SQ Sequence 231 AA; | SQ Sequence 231 AA; |
| Query Match 85.1%; Score 1218; DB 22; Length 231; | Query Match 85.1%; Score 1218; DB 22; Length 231; |
| Best Local Similarity 87.8%; Pred. No. 1.5e-113; | Best Local Similarity 87.8%; Pred. No. 1.5e-113; |
| Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1; | Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1; |
| Qy 1 MNPXKCFGLISFLLTGAGTQSTHESLKPRVQFQSRNFHNLQWPGRALTGNSVY 60 | Qy 1 MNPXKCFGLISFLLTGAGTQSTHESLKPRVQFQSRNFHNLQWPGRALTGNSVY 60 |
| Db 1 MNPXKCFGLISFLLTGAGTQSTHESLKPRVQFQSRNFHNLQWPGRALTGNSVY 60 | Db 1 MNPXKCFGLISFLLTGAGTQSTHESLKPRVQFQSRNFHNLQWPGRALTGNSVY 60 |
| Qy 61 FVQYKMFSCMSKSHQPSGQWHISCNFPCGRTLAKYQORQWKNKEDCWGTQELSDDL 120 | Qy 61 FVQYKMFSCMSKSHQPSGQWHISCNFPCGRTLAKYQORQWKNKEDCWGTQELSDDL 120 |
| Db 61 FVQYKI-----YQORQWKNKEDCWGTQELSDDL 88 | Db 61 FVQYKI-----YQORQWKNKEDCWGTQELSDDL 88 |
| Qy 121 TSETSDIOEPYVGRVRAASAGYSWSMTPTPTWETKIDPPVNNITQVNGSLVLVHA 180 | Qy 121 TSETSDIOEPYVGRVRAASAGYSWSMTPTPTWETKIDPPVNNITQVNGSLVLVHA 180 |
| Db 89 TSETSDIOEPYVGRVRAASAGYSWSMTPTPTWETKIDPPVNNITQVNGSLVLVHA 148 | Db 89 TSETSDIOEPYVGRVRAASAGYSWSMTPTPTWETKIDPPVNNITQVNGSLVLVHA 148 |
| Qy 181 PNLFPYQKKNVSTIEDYELLRYVFIINNSLEKEQKYVEGAHRAVEIEALTPHSSYCV 240 | Qy 181 PNLFPYQKKNVSTIEDYELLRYVFIINNSLEKEQKYVEGAHRAVEIEALTPHSSYCV 240 |
| Db 149 PNLFPYQKKNVSTIEDYELLRYVFIINNSLEKEQKYVEGAHRAVEIEALTPHSSYCV 208 | Db 149 PNLFPYQKKNVSTIEDYELLRYVFIINNSLEKEQKYVEGAHRAVEIEALTPHSSYCV 208 |
| Qy 241 AEIYQPMLDRRSQSRSEECVIEP 263 | Qy 241 AEIYQPMLDRRSQSRSEECVIEP 263 |
| Db 209 AEIYQPMLDRRSQSRSEECVIEP 231 | Db 209 AEIYQPMLDRRSQSRSEECVIEP 231 |
| RESULT 7 | |

QY 61 FVOYKIMFSCMSKSHQSPSCWQHISCNFPGCRRLAKYGORWKNKEDCWGTOLSCDL 120
 Db 61 FVOYKI-----YGORWKNKEDCWGTOLSCDL 88
 QY 121 TSETSDIQEPPYGRVRAASAGSYSEWSMTFRFTPWETKIDPPVNNITQVNGSLVILHA 180
 Db 89 TSETSDIQEPPYGRVRAASAGSYSEWSMTFRFTPWETKIDPPVNNITQVNGSLVILHA 148
 QY 181 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240
 Db 149 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 208
 QY 241 AEIYQPMLDRRSQRSEERCVEIP 263
 Db 209 AEIYQPMLDRRSQRSEERCVEIP 231
 RESULT 8
 ID AAB62657 standard; Protein; 231 AA.
 AC AAB62657;
 XX
 DT 23-JUL-2001 (first entry)
 DE Human cytokine receptor, zcytor16.
 XX
 KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
 KW antiarthritis; antiarthritic; antiasthmatic; antiatherosclerotic;
 KW immunosuppressive; chromosome 6q24.1-25.2; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 22..108 /note= "Ig domain 1"
 FT Domain 22..231 /note= "extracellular domain"
 FT Domain 112..210 /note= "Ig domain 2"
 XX
 PN WO200140467-A1.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US32703.
 XX
 PR 03-DEC-1999; 99US-0169049.
 PR 13-SEP-2000; 2000US-0232219.
 PR 31-OCT-2000; 2000US-0244610.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
 XX
 DR WPI; 2001-356158/37.
 DR N-PSDS; AAF83735.
 XX
 PT New soluble cytokine receptor polypeptides and polynucleotides, useful
 XX for diagnosing and treating cancer and inflammatory conditions -
 PS Claim 1; Page 186-188; 210pp; English.
 XX
 CC The invention relates to a human cytokine receptor polypeptide,
 CC designated zcytor16. The zcytor16 polypeptide can be expressed by
 CC standard recombinant methodology and can bind to IL-TIF (undefined). The
 CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
 CC or differentiation of hematopoietic cell(s) (progenitors); reducing
 CC IL-TIF induced or IL-9 induced inflammation; and suppressing an
 CC inflammatory response in a mammal with inflammation. Heteromeric/
 CC multimeric receptor polypeptides such as soluble zcytor 16/CRP2-4 can be
 CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides

CC can also be used to detect IL-TIF levels which is indicative of
 CC pathological conditions including inflammatory states (e.g. rheumatoid
 CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
 CC polypeptides themselves are useful for the treatment of inflammation,
 CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel
 CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune
 CC diseases. The antibodies and zcytor16 polynucleotides are also useful
 CC for detecting cancer. The present sequence represents the human
 CC zcytor16 protein.

XX SQ Sequence 231 AA;

Query Match 85.1%; Score 1218; DB 22; Length 231;
 Best Local Similarity 87.8%; Pred. No. 1.5e-113;
 Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MPPKHCFLGLISFFLTGVAGTOSTHESLKPQVQFOSRNFHNLQWPGRALTGNSVY 60

Db 1 MPPKHCFLGLISFFLTGVAGTOSTHESLKPQVQFOSRNFHNLQWPGRALTGNSVY 60

QY 61 FVOYKIMFSCMSKSHQSPSCWQHISCNFPGCRRLAKYGORWKNKEDCWGTOLSCDL 120

Db 61 FVOYKI-----YGORWKNKEDCWGTOLSCDL 88

QY 121 TSETSDIQEPPYGRVRAASAGSYSEWSMTFRFTPWETKIDPPVNNITQVNGSLVILHA 180

Db 89 TSETSDIQEPPYGRVRAASAGSYSEWSMTFRFTPWETKIDPPVNNITQVNGSLVILHA 148

QY 181 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 240

Db 149 PNLPRYQKEKNVSIEDYELLYRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVV 208

QY 241 AEIYQPMLDRRSQRSEERCVEIP 263

Db 209 AEIYQPMLDRRSQRSEERCVEIP 231

RESULT 9

ID AAE28600 standard; Protein; 231 AA.

XX AAE28600;

XX 27-DEC-2002 (first entry)

DE Human Zcytor16 protein.

XX Cytokine receptor; Zcytor16; IL-TIF; autoimmune disease; dermatological;
 KW inflammatory disease; inflammatory bowel disease; rheumatoid arthritis;
 KW asthma; systemic lupus erythematosus; myasthenia gravis; pancreatitis;
 KW diabetes; atherosclerosis; glomerulonephritis; gene therapy; cytostatic;
 KW immunosuppressive; nephrotropic; allergy; placental health; abortion;
 KW cancer; human; chromosome 6.

OS Homo sapiens.

FH Key Location/Qualifiers
 FT Peptide 1..22 /label= Signal_peptide
 FT Protein 23..231 /note= "Mouse mature Zcytor16 protein"
 FT Domain 32..123 /note= "Fibronectin III domain I"
 FT Domain 32..230 /note= "Cytokine binding domain"
 FT Region 124..131 /note= "Linker"
 FT Domain 132..230 /note= "Fibronectin III domain II"
 FT Domain 220..223 /note= "Class II cytokine domain"
 XX

PN WO200270655-A2.

```

XX PD 12-SEP-2002.
XX XX
XX PF 04-MAR-2002; 2002WO-US06267.
XX XX
XX PR 02-MAR-2001; 2001US-273035P.
XX PR 27-MAR-2001; 2001US-279232P.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX XX
XX PI Presnell SR, Xu W, Kindevogel W, Chen Z;
XX XX
XX DR WPI; 2002-698750/75.
XX DR N-PSDB; AAD45959.
XX XX
XX PT New Zcytor16 polypeptide useful for treating autoimmune or inflammatory
XX PT diseases, e.g. inflammatory bowel disease, rheumatoid arthritis,
XX PT asthma, atherosclerosis, cancer or diabetes, or in assessing
XX PT therapeutic aspects of IL-TIF
XX XX
XX PS Example 1; Page 191; 221pp; English.
XX XX
XX CC The invention relates to cytokine receptor designated as mouse Zcytor16
XX CC which can bind and antagonize the IL-TIF. The Zcytor16 polypeptide is
XX CC useful in modulating the immune system by binding Zcytor16 ligand, and
XX CC thus, preventing the binding of the ligand with endogenous Zcytor16
XX CC receptor. It is useful for studying human inflammation or immune
XX CC function, or for treating autoimmune or inflammatory diseases such as
XX CC inflammatory bowel disease, rheumatoid arthritis, asthma, systemic
XX CC lupus erythematosus, myasthenia gravis or allergy, atherosclerosis,
XX CC cancer, diabetes, glomerulonephritis or pancreatitis, or in assessing
XX CC therapeutic aspects of IL-TIF, chemical therapeutics, anti-IL-TIF
XX CC antibodies, anti-Zcytor16 antibodies or Zcytor16 soluble receptors.
XX CC Zcytor16 DNA and the anti-mouse Zcytor16 antibody are useful as probes
XX CC in detecting gene expression and gene structure, such as in the
XX CC diagnosis and/or prevention of spontaneous abortions or in monitoring
XX CC placental health and function. It is also used in gene therapy. The
XX CC present sequence is human Zcytor16 protein. Human Zcytor16 gene resides
XX CC at chromosome 6.
XX XX
XX SQ Sequence 231 AA;
XX XX
XX Query Match 85.1%; Score 1218; DB 23; Length 231;
XX XX Best Local Similarity 87.8%; Pred. No. 1.5e-113;
XX XX Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
XX XX
QY 1 MNPKHCFGLGISFFLTGVAGTQSTHESLKPQVQFSRNFHNLQWPGRALTGNSVY 60
DB 1 MNPKHCFGLGISFFLTGVAGTQSTHESLKPQVQFSRNFHNLQWPGRALTGNSVY 60
QY 61 FVQYKIMFSCSMKSSHQKPSGCGWHISCNPPGCTLAKYQORWKNKDCWGTOELSCDL 120
DB 61 FVQYKI-----YQORWKNKDCWGTOELSCDL 88
QY 121 TSSTSDIQBPYGRVRAASAGSYSEWSMTFRPTPWNETKIDPPVMNITQVNGSLVLHA 180
DB 89 TSSTSDIQBPYGRVRAASAGSYSEWSMTFRPTPWNETKIDPPVMNITQVNGSLVLHA 148
QY 181 PNLPRYQKEKNVSIEDYELLRYRVIINNSLEKEQKVYEGAHRAVEIALTPHSSYCVV 240
DB 149 PNLPRYQKEKNVSIEDYELLRYRVIINNSLEKEQKVYEGAHRAVEIALTPHSSYCVV 208
QY 241 AEIYQPMLDRRRSQSRSERCVEIP 263
DB 209 AEIYQPMLDRRRSQSRSERCVEIP 231
XX XX
XX RESULT 10
XX ABJ010498
XX ID ABJ010498 standard; Protein; 231 AA.
XX XX
XX AC ABJ010498;
XX XX

```

```

DT 21-NOV-2002 (first entry)
XX XX
XX DE Cytokine receptor family 2 (CRF2) related protein SEQ ID No 2.
XX KW Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
XX KW antiinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;
XX KW gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;
XX KW interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;
XX KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
XX KW inflammation.
XX OS Unidentified.
XX XX
XX PN WO200266647-A2.
XX XX
XX PD 29-AUG-2002.
XX XX
XX PF 14-JAN-2002; 2002WO-US00986.
XX XX
XX PR 12-JAN-2001; 2001US-261442P.
XX PR 06-FEB-2001; 2001US-267021P.
XX PR 23-FEB-2001; 2001US-270835P.
XX XX
XX PA (GEMY ) GENETICS INST LLC.
XX XX
XX PI Fouser L, Liu W, Deng B;
XX XX
XX DR WPI; 2002-674946/72.
XX DR N-PSDB; ABT08216.
XX XX
XX PT New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for
XX PT diagnosing and treating disorders with abnormal CRF2-12 activity such
XX PT as autoimmune diseases like rheumatoid arthritis, multiple sclerosis
XX PT and inflammation
XX XX
XX PS Claim 2; Page 6; 91pp; English.
XX XX
XX CC The invention relates to an isolated type 2 cytokine receptor family
XX CC (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids
XX CC 21-66 of a 231 residue amino acid sequence, given in the specification,
XX CC or its complement. The compositions and methods of the present invention
XX CC are useful for diagnosing, screening and treating disorders associated
XX CC with abnormal CRF2-12 activity such as autoimmune diseases like
XX CC rheumatoid arthritis, multiple sclerosis and inflammation. This sequence
XX CC represents a cytokine receptor family 2 (CRF2-12) protein relating to the
XX CC invention.
XX XX
XX SQ Sequence 231 AA;
XX XX
XX Query Match 85.1%; Score 1218; DB 23; Length 231;
XX XX Best Local Similarity 87.8%; Pred. No. 1.5e-113;
XX XX Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
XX XX
QY 1 MNPKHCFGLGISFFLTGVAGTQSTHESLKPQVQFSRNFHNLQWPGRALTGNSVY 60
DB 1 MNPKHCFGLGISFFLTGVAGTQSTHESLKPQVQFSRNFHNLQWPGRALTGNSVY 60
QY 61 FVQYKIMFSCSMKSSHQKPSGCGWHISCNPPGCTLAKYQORWKNKDCWGTOELSCDL 120
DB 61 FVQYKI-----YQORWKNKDCWGTOELSCDL 88
QY 121 TSSTSDIQBPYGRVRAASAGSYSEWSMTFRPTPWNETKIDPPVMNITQVNGSLVLHA 180
DB 89 TSSTSDIQBPYGRVRAASAGSYSEWSMTFRPTPWNETKIDPPVMNITQVNGSLVLHA 148
QY 181 PNLPRYQKEKNVSIEDYELLRYRVIINNSLEKEQKVYEGAHRAVEIALTPHSSYCVV 240
DB 149 PNLPRYQKEKNVSIEDYELLRYRVIINNSLEKEQKVYEGAHRAVEIALTPHSSYCVV 208
QY 241 AEIYQPMLDRRRSQSRSERCVEIP 263
DB 209 AEIYQPMLDRRRSQSRSERCVEIP 231
XX XX

```

QY 1 MNPKHCFGLFLISFFLTGTGAGTQSTHESLKPQVQFOSRNFHNLQWQGRALTGNSVY 60

Db 1 MMPKCHFLGLISFLTLVAGTQSTHESLKPQVQFQSRNPHNLOQPGRLTGNSSVY 60
 QY 61 FVOYKIMFSCMKSHQKPSGCWQHISCNFPQCTLAKYQORQWKNKEDCWGTQELSCDL 120
 Db 61 FVOYKI-----YQORQWKNKEDCWGTQELSCDL 88
 QY 121 TSETSDIQEPPYGRVRAASAGSYSEWSMTFRFTPWETKIDPPVNNITQVNGSLVILHA 180
 Db 89 TSETSDIQEPPYGRVRAASAGSYSEWSMTFRFTPWETKIDPPVNNITQVNGSLVILHA 148
 QY 181 PNLPRYQKQKNSIEDYELLYRVFIINNSLEKEQKVYEGAHRAVEIALTPHSSYCVV 240
 Db 149 PNLPRYQKQKNSIEDYELLYRVFIINNSLEKEQKVYEGAHRAVEIALTPHSSYCVV 208
 QY 241 AEIYQPMLEDRRSQSERCVEIP 263
 Db 209 AEIYQPMLEDRRSQSERCVEIP 231

RESULT 13
 ABG34086

ID ABG34086 standard; Protein; 231 AA.

XX AC ABG34086;

DT 15-JUL-2002 (first entry)

XX Human Pro peptide #57.

XX Human; PRO; secreted protein; transmembrane protein;

XX genetic disorder; tumour; cancer.

XX Homo sapiens.

PN WO200224888-A2.

XX 28-MAR-2002.

XX 29-AUG-2001; 2001WO-US27059.

XX 01-SEP-2000; 2000US-229896P.

PR 05-SEP-2000; 2000US-230621P.

PR 22-SEP-2000; 2000US-235147P.

PR 10-NOV-2000; 2000WO-US3087P.

PR 12-JAN-2001; 2001US-261878P.

PR 16-JAN-2001; 2001US-261910P.

PR 16-JAN-2001; 2001US-261939P.

PR 25-JAN-2001; 2001US-262150P.

PR 02-FEB-2001; 2001US-264395P.

PR 08-FEB-2001; 2001US-266421P.

PR 28-FEB-2001; 2001US-267623P.

PR 09-MAR-2001; 2001US-274399P.

PR 03-APR-2001; 2001US-280982P.

PR 04-APR-2001; 2001US-282129P.

PR 09-MAY-2001; 2001US-282199P.

PR 25-MAY-2001; 2001WO-US17092.

PR 01-JUN-2001; 2001WO-US17800.

PR 20-JUN-2001; 2001WO-US19692.

PR 29-JUN-2001; 2001WO-US21066.

PR 09-JUL-2001; 2001WO-US21735.

PA (GETH) GENENTECH INC.

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;

PI Fong S;

XX WPI; 2002-362426/39.

DR N-PSDB; ABK70017.

XX New PRO polypeptides and polynucleotides encoding the polypeptides,

PT

PT useful in gene therapy, chromosome identification, tissue typing, or
 PT for genetic analysis of individuals with genetic disorders -
 XX Claim 11; Figure 114; 219pp; English.

XX This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The
 CC invention also comprises a method for producing the proteins of the
 CC invention by recombinant means and antibodies specific for the protein
 CC of the invention. The antibody may be used for detecting the PRO
 CC proteins of the invention and may be used to modify their activity.
 CC polynucleotides may be used as hybridisation probes for a cDNA library
 CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to
 CC construct hybridisation probes for mapping the gene which encodes that
 CC PRO and for genetic analysis of individuals with genetic disorders, in
 CC assays to identify other proteins or molecules involved in binding
 CC reaction, to generate transgenic animals or knock-out animals which in
 CC turn are useful in the development and screening of therapeutically
 CC useful reagents, for chromosome identification, and as tissue typing. The
 CC PRO polypeptides are useful in gene therapy, and as molecular weight
 CC markers for protein electrophoresis purposes. The sequences may
 CC also be used to detect overexpression on PRO polypeptides in cancerous
 CC tumours and for screening for differentially expressed genes using
 CC microarray technology. The present sequence represents a human PRO
 CC protein of the invention.

XX SQ Sequence 231 AA;

Query Match 85.1%; Score 1218; DB 23; Length 231;

Best Local Similarity 87.8%; Pred. No. 1.5e-113;

Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MMPKCHFLGLISFLTLVAGTQSTHESLKPQVQFQSRNPHNLOQPGRLTGNSSVY 60

Db 1 MMPKCHFLGLISFLTLVAGTQSTHESLKPQVQFQSRNPHNLOQPGRLTGNSSVY 60

QY 61 FVOYKIMFSCMKSHQKPSGCWQHISCNFPQCTLAKYQORQWKNKEDCWGTQELSCDL 120

Db 61 FVOYKI-----YQORQWKNKEDCWGTQELSCDL 88

QY 121 TSETSDIQEPPYGRVRAASAGSYSEWSMTFRFTPWETKIDPPVNNITQVNGSLVILHA 180

Db 89 TSETSDIQEPPYGRVRAASAGSYSEWSMTFRFTPWETKIDPPVNNITQVNGSLVILHA 148

QY 181 PNLPRYQKQKNSIEDYELLYRVFIINNSLEKEQKVYEGAHRAVEIALTPHSSYCVV 240

Db 149 PNLPRYQKQKNSIEDYELLYRVFIINNSLEKEQKVYEGAHRAVEIALTPHSSYCVV 208

QY 241 AEIYQPMLEDRRSQSERCVEIP 263

Db 209 AEIYQPMLEDRRSQSERCVEIP 231

RESULT 14

AAE17320

ID AAE17320 standard; Protein; 231 AA.

XX AC AAE17320;

DT 18-APR-2002 (first entry)

DE Human cytokine receptor protein, sbg456548Cytora #2.

XX Human; therapy; wound healing disorder; vaccine; cancer; infection;

KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;

KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;

KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;

KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;

KW depression; cardiovascular disease; myocardial infarction; renal failure;

KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;

KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;

KW hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease;

KW neutropenic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;

KW haemostatic; vulnary; anticonvulsant; antirheumatic; neuroprotective;
 KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
 KW allergy; cytokine receptor.
 XX Homo sapiens.
 XX WO200198342-A1.
 XX 27-DEC-2001.
 XX 22-JUN-2001; 2001WO-US19929.
 XX 22-JUN-2000; 2000US-213156P.
 XX 22-JUN-2000; 2000US-213161P.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX (GLAX) GLAXO GROUP LTD.
 XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
 PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
 XX N-PSDB; AAD27815.
 DR WPI; 2002-139783/18.
 DR N-PSDB; AAD27815.
 XX Novel secreted and membrane-associated polypeptides and polynucleotides
 PT useful for preventing, ameliorating or correcting dysfunction or
 PT disease including diabetes, cancer, hypertension and growth
 PT abnormalities -
 XX Claim 1; Page 132-133; 138pp; English.
 XX The invention relates to secreted and membrane-associated polypeptides
 CC and polynucleotides. The sequences of the invention are useful in
 CC diagnostic assays for detecting diseases associated with inappropriate
 CC activity or levels of these polynucleotides, and in identifying their
 CC agonists and antagonists that are potentially useful in therapy. The
 CC sequences of the invention are useful as vaccines for inducing
 CC immunological response. The sequences of the invention are useful for
 CC treating cancers, infections, autoimmune disorders, haematopoietic
 CC disorders, wound healing disorders, cholesterol ester storage disease,
 CC inflammation, congenital muscular dystrophy, junctional epidermolysis
 CC bullosa, Bacterial's disease, Huntington's chorea, multiple sclerosis,
 CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
 CC allergies, schizophrenia, sbg442445PROA-associated disorders,
 CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,
 CC graft verse host disease, ischaemia, stroke, acute respiratory disease,
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,
 CC brain disorders including paraspranuclear palsy, myotonic dystrophy,
 CC depression, anxiety disorders and sleep disorders, cardiovascular
 CC diseases including congestive heart failure and myocardial infarction,
 CC respiratory diseases including chronic obstructive pulmonary disease,
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders
 CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
 CC and tendinitis, gastrointestinal diseases including intestinal
 CC obstruction and tropical sprue, spleen disorders including hyperplenism,
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
 CC reproductive diseases including low testosterone and male infertility.
 CC The present sequence is human cytokine receptor.
 XX

SQ Sequence 231 AA;

Query Match 85.1%; Score 1218; DB 23; Length 231;
 Best Local Similarity 87.8%; Pred. No. 1.5e-113;
 Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MNPKHCFGLFGLISFFLTGAGTOSTHSLKQRFQFQSRFHNILQWQPGALTGNSVY 60
 DB 1 MNPKHCFGLFGLISFFLTGAGTOSTHSLKQRFQFQSRFHNILQWQPGALTGNSVY 60

QY 61 FVQYKIMFSCMKSSHQKPSGCWQHISCNPPGCRITLAKYQROWKNKEDCWGTLSDDL 120
 DB 61 FVQYKIMFSCMKSSHQKPSGCWQHISCNPPGCRITLAKYQROWKNKEDCWGTLSDDL 88
 QY 121 TSSTSDIQEPPYQYGRVRAASAGSYSEWSMTFRFTPMWETKIDPPVMNITQVNGSLVILHA 180
 DB 89 TSSTSDIQEPPYQYGRVRAASAGSYSEWSMTFRFTPMWETKIDPPVMNITQVNGSLVILHA 148
 QY 181 PNLPRYQKEKNVSIEDYVELLYRVFIINNSLSEKQKVEGAHRAVEIEALTTHSSYCVV 240
 DB 149 PNLPRYQKEKNVSIEDYVELLYRVFIINNSLSEKQKVEGAHRAVEIEALTTHSSYCVV 208
 QY 241 AEIYQPMLEDRSQRSEERCVEIP 263
 DB 209 AEIYQPMLEDRSQRSEERCVEIP 231
 RESULT 15
 AAE30826
 ID AAE30826 standard; Protein; 231 AA.
 AC AAE30826;
 XX 24-FEB-2003 (first entry)
 XX Human cytokine receptor, Zcytor16 protein.
 DE Human; cytokine receptor; Zcytor16; immune function; autoimmune disease;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; asthma;
 KW arthritis; psoriasis; endotoxaemia; septicemia; toxic shock syndrome;
 KW infectious disease; cancer; diabetes; renal dysfunction; pancreatitis;
 KW spontaneous abortion; placental health; gene therapy; nephrotropic;
 KW chromosome 6q23-q24.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 XX Peptide 1..22 /label= Signal_peptide
 FT Protein 23..231 /notes= Mature human Zcytor16 protein"
 FT Domain 32..123 /notes= "Fibronectin III domain I"
 FT Domain 132..230 /notes= "Fibronectin III domain II"
 FT Region 128..131 /notes= "Linker peptide"
 FT WO200277174-A2.
 XX 03-OCT-2002.
 XX 22-MAR-2002; 2002WO-US08811.
 XX 27-MAR-2001; 2001US-279222P.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Presnell SR, Xu W, Kindsvogel W, Chen Z, Hughes SD;
 XX WPI; 2003-029924/02.
 XX N-PSDB; AAD48049.
 XX New Zcytor16 polypeptide useful for treating or detecting autoimmune or
 PT inflammatory diseases, e.g. inflammatory bowel disease, arthritis,
 PT asthma, diabetes, cancer, psoriasis, endotoxaemia, septicemia, or
 PT infectious diseases -
 XX Claim 3; Page 233-234; 268pp; English.
 XX The invention relates to cytokine receptor polypeptide, Zcytor16. The
 CC polypeptide is useful in modulating the immune system by binding Zcytor16
 CC ligand and thus preventing the binding of the ligand with endogenous

CC Zcytor16 receptor. It is useful for studying human inflammation or immune
CC function, or for treating autoimmune or inflammatory diseases such as
CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC arthritis, psoriasis, endotoxaemia, septicemia, toxic shock syndrome or
CC infectious disease, asthma, cancer, diabetes, renal dysfunctions or
CC pancreatitis or in assessing therapeutic aspects of IL-1RIF, chemical
CC therapeutics, anti-IL-1RIF antibodies, anti-Zcytor16 antibodies or
CC Zcytor16 soluble receptors. The nucleic acid molecule and the antibody
CC are useful as probes in detecting gene expression and gene structure,
CC such as in the diagnosis and/or prevention of spontaneous abortions or
CC in monitoring placental health and function. The invention is useful in
CC gene therapy. The present sequence is human Zcytor16 protein. Zcytor16
CC gene is located on chromosome 6q23-q24.

XX
SQ Sequence 231 AA;

Query Match 85.1%; Score 1218; DB 24; Length 231;
Best Local Similarity 87.8%; Pred. No. 1.5e-113;
Matches 231; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MMEKHCFLGLISFLLTGAGTOSTHESLKPQRVQFSRNFHNILOWQGRALTGNSVY 60
DB 1 MMEKHCFLGLISFLLTGAGTOSTHESLKPQRVQFSRNFHNILOWQGRALTGNSVY 60

QY 61 FVQYKIMFSCMKSHQKPSGCWQHISCNPPGCRTLAKYQQRQWKNKEDCWGTQELS CDL 120
DB 61 FVQYKI-----YQQRQWKNKEDCWGTQELS CDL 88

QY 121 TSSTSDIQBPYGRVRAAGSAGSYSEWSMTPTPTPWETKIDPPVMNITQVNGSLVLVILHA 180
DB 89 TSSTSDIQBPYGRVRAAGSAGSYSEWSMTPTPTPWETKIDPPVMNITQVNGSLVLVILHA 148

QY 181 PNLPHYQKEKNYSIEDYVELLYRVFIINNSLEKQKVEGAHRAVEIEALTPHSSYCVV 240
DB 149 PNLPHYQKEKNYSIEDYVELLYRVFIINNSLEKQKVEGAHRAVEIEALTPHSSYCVV 208

QY 241 AIIYQPMLDRRRSORSEERCVEIP 263
DB 209 AIIYQPMLDRRRSORSEERCVEIP 231

Search completed: December 12, 2003, 12:25:33
Job time : 67.8644 secs

Query Match 21.7%; Score 311; DB 2; Length 221;
 Best Local Similarity 32.0%; Pred. No. 1.7e-27;
 Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 30 KQORVQFSRNFHNILOQPCGRALTGNSVYFVQYKIMFSCSMKSHQKPGSCWQHISCN 89
 DB 10 KPGNITFSLNKNVLTQTPPEGLQGVKVTYVQYFI----- 46
 QY 90 FPGCRTLAKYQOROWKNKEDCGTQELSCDLTSETSDIQEPIYGRVRAASAGSYSEWSMT 149
 DB 47 -----YQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTCCKSWAES 97
 QY 150 PRFTPMWETKIDPPVMNITQVNGSLVLHAPNLPYRQKKNVSIEDYY-ELLYRVFII 208
 DB 98 GRFYFPLETQIGPPEVGLTTDEKSI SVLTAPKWKRNPEDLPVSMQIYSLNLYNSVL 157
 QY 209 NNSLEKEQKVEGAHRAVEIEALTPHSSYCVVAEIQMFLDRRSORSERC 259
 DB 158 NTKSNRTWSQCVTNHTLV-LTWLEPTLYCVHVESFVPGPPRRAQPSKQC 207

RESULT 2
 US-08-943-087-50
 ; Sequence 50, Application US/08943087
 ; Patent No. 5945511
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; APPLICANT: Kho, Choon J.
 ; APPLICANT: Jelmeberg, Anna C.
 ; APPLICANT: Adams, Robyn L.
 ; APPLICANT: Whitmore, Theodore E.
 ; APPLICANT: Farrah, Theresa M.
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZymoGenetics, Inc.
 ; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/943,087
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/803,305
 ; FILING DATE: 20-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lunn, Paul G
 ; REGISTRATION NUMBER: 32,743
 ; REFERENCE/DOCKET NUMBER: 96-24C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6627
 ; TELEFAX: 206-442-6678
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 221 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-943-087-50

Query Match 21.6%; Score 310; DB 2; Length 221;
 Best Local Similarity 32.0%; Pred. No. 2.2e-27;

Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

QY 30 KQORVQFSRNFHNILOQPCGRALTGNSVYFVQYKIMFSCSMKSHQKPGSCWQHISCN 89
 DB 10 KPGNITFSLNKNVLTQTPPEGLQGVKVTYVQYFI----- 46
 QY 90 FPGCRTLAKYQOROWKNKEDCGTQELSCDLTSETSDIQEPIYGRVRAASAGSYSEWSMT 149
 DB 47 -----YQKKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIWGTCCKSWAES 97
 QY 150 PRFTPMWETKIDPPVMNITQVNGSLVLHAPNLPYRQKKNVSIEDYY-ELLYRVFII 208
 DB 98 GRFYFPLETQIGPPEVGLTTDEKSI SVLTAPKWKRNPEDLPVSMQIYSLNLYNSVL 157
 QY 209 NNSLEKEQKVEGAHRAVEIEALTPHSSYCVVAEIQMFLDRRSORSERC 259
 DB 158 NTKSNRTWSQCVTNHTLV-LTWLEPTLYCVHVESFVPGPPRRAQPSKQC 207

RESULT 3
 US-08-943-087-56
 ; Sequence 56, Application US/08943087
 ; Patent No. 5945511
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; APPLICANT: Kho, Choon J.
 ; APPLICANT: Jelmeberg, Anna C.
 ; APPLICANT: Adams, Robyn L.
 ; APPLICANT: Whitmore, Theodore E.
 ; APPLICANT: Farrah, Theresa M.
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZymoGenetics, Inc.
 ; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/943,087
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/803,305
 ; FILING DATE: 20-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lunn, Paul G
 ; REGISTRATION NUMBER: 32,743
 ; REFERENCE/DOCKET NUMBER: 96-24C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6627
 ; TELEFAX: 206-442-6678
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 221 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-943-087-56

Query Match 21.6%; Score 310; DB 2; Length 221;
 Best Local Similarity 31.6%; Pred. No. 2.2e-27;
 Matches 73; Conservative 34; Mismatches 90; Indels 34; Gaps 3;

| | | | |
|----|-----|--|-----|
| Qy | 30 | KPQRVQSRNFHILQWPGALTGNSVTFVQYKIMFSCSMKSHOKPSCGWQHISCN | 89 |
| Db | 10 | KPANIITFSLINMKNVLWTPPEGLQGVKVTYTVQYFI | 46 |
| Qy | 90 | PPGCRITLAKYQORQWKNEKCGWQELSCDITSETSDIQEPPYGVRAASAGSYSEWSMT | 149 |
| Db | 47 | -----YQCKWLNKSECRINRTYCDLSAETSDYEHQYAKVKAIGWSKCSKWAES | 97 |
| Qy | 150 | PRFTPWETKIDPPVMNITQVNGSLLVILHAPNLPYRQKEKNVSIEDYY-BLLYRVFTII | 208 |
| Db | 98 | GRFYFFLESQIGPPEVALTSDKISIVSVLSAPEKWKRNPEDLPSVMQOIYSNLKTVNSVL | 157 |
| Qy | 209 | NNSLEKQKVYEGAHRAVEIBALTPHSSYCVVAEIIYQPLDRRSQRSERC | 259 |
| Db | 158 | NTKSNRTWSOCVNTHTLV-LTWLEPNTLYCVHVESFVPGPPRAAPSEKOC | 207 |

RESULT 4
 US-08-943-087-2
 ; Sequence 2, Application US/08943087
 ; Patent No. 5945511
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; APPLICANT: Kho, Choon J.
 ; APPLICANT: Jelmberg, Anna C.
 ; APPLICANT: Adams, Robyn L.
 ; APPLICANT: Whitmore, Theodore E.
 ; APPLICANT: Farrah, Theresa M.
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZymoGenetics, Inc.
 ; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA: US/08/943,087
 ; APPLICATION NUMBER: US/08/943,087
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/803,305
 ; FILING DATE: 20-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lunn, Paul G
 ; REGISTRATION NUMBER: 32,743
 ; REFERENCE/DOCKET NUMBER: 96-24C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6627
 ; TELEFAX: 206-442-6678
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 553 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ;
 US-08-943-087-2
 Query Match 21.6%; Score 310; DB 2; Length 553;
 Best Local Similarity 32.0%; Pred.No. 9.3e-27;
 Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;
 30 KPQRVQFSRNFNIILOWQPGRALTGNSSVYFVQYKIMFSCMKSSHQKPGCGWHISCN 89

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Db      39  K P A N I T F L S I N K N V L O W T P E G L O G V K V T Y T V O Y F I . . . . . 75
Qy      90  F P O C R T L A K Y G O R Q W K N K E D C W G T Q E L S C D L T S E T S I O E P Y G R V R A A S G S Y S E W S M T 149
Db      76  -----Y G Q K K W L N K S C R N I N R T Y C D L S A E T S D Y E H O Y A K V K A I W G T K C S K W A E S 126
Qy      150  P R E T P W E T K I D P P V M N I T O V N G S L L V I L H A P N L P Y R O K E K N Y S I E D Y Y - E L L Y R V F I I 208
Db      127  G R Y P F L E T O I G P P E V A L T T D E K S I S V L T A P E K W K N P E D L P S M Q O I Y N L N K N V S V L 186
Qy      209  N S L E K E Q K Y V E G A H R A V E I A L T P H S S Y C V W A I Y O P M L D R R S Q R S E E R C 259
Db      187  N T K S N R T S Q C V T N H T I V - L T W L E P N T L Y C V H V E S F V G P P R R A Q P S E K Q C 236

RESULT 5
US-08-943-087-14
; Sequence 14, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102

```

RESULT 5

```

US-08-943-087-14
Sequence 14, Application US/08943087
Patent No. 5945511
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Kho, Choon J.
APPLICANT: Jelmsberg, Anna C.
APPLICANT: Adams, Robyn L.
APPLICANT: Whitmore, Theodore B.
APPLICANT: Fairhair, Theresa M.
TITLE OF INVENTION: CYTOKINE REC
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue E
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/803,305
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lumu, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-943-087-14

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Query Match      21.6%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches       74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;
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QY    30 KPORVQFSRNFHNILQWPGRLTNGSVFYVQYKIMFSCSMKSSHQKPSGCWGQHISCN 89
      :|::|||:|||||
Db     39 KPANIFFLSINKKNVLQMTPEEGLOGVKYTYTVQYEI-----75
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Qy 30 KPQRVQFQSRNFHNLQWOPGRALTGNSSVFYVQVKIMFSCSMKSSHQKPSGCGQHISCN 89
|| : ||| | : ||| | : ||| |
Dd 39 KPNITFLINMKRVLOWTPPEGLGKVTVTVQYFI----- 75

| | | | |
|----|-----|--|-----|
| Db | 76 | -----YQKKWLNSCRNTRNTYCDLSAETSDYHQYAKVKAIGWTKCSKWAES | 126 |
| QY | 150 | PRFTPWETKIDPPVMNITQVNGSLLVILHAPNLPYRQKEKNYSIEDYY-ELLRYVFII | 208 |
| Db | 127 | GREYFPLETQIGPPEVALTTDEKSIISVLTAPEKWKKNPEPLPVSQQOYISNLYKNVSVL | 186 |
| QY | 209 | NNSLEKEQKYVGEAHRAVEATEALTPHSSYCVVAEIQPMLDRRSORSERC | 259 |
| Db | 187 | NTKSNRTWSOCVNTHTLV-LTWLEPNTLYCVHVESFVGGPERRAQPSKQC | 236 |

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RESULT 7
US-08-943-087-18
; Sequence 18, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536

```

PRIOR APPLICATION DATA: 08/803,305
 APPLICATION NUMBER: 08/803,305
 FILING DATE: 20-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-24CI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX:
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 553 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-08-943-087-18

```

Query Match      21.6%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches         74; Conservative 33; Mismatches 90; Indels 34; Gaps 3

30 KPORVQFOSRNPHNIILOQPGRALTGNSSVFYVQYKIMFSCSMKSSHQKPSGCWHISCN 89
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db

39 KPANITFLSINMKNVLIOWTPPEGLQGVKYTYTVQYFI----- 75

90 FPGCETLAKYGORWNKNEDCWGTQLSDLTSETSDIQBPYTCRVFAAAGSYSEWSMT 149
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db

76 -----YGOKKWLNKSECNRINNTYCDLSAETSDEHYQYAKVAIKWGTCKSKWAES 126

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```
Query Match      21.6%; Score 310; DB 2; Length 553;  
Best Local Similarity 32.0%; Pred. No. 9,3e-27;  
Matches       74; Conservative 33; Mismatches 90; Indels   34; Gaps    3
```



```
QY          30 KPRVQFSRNFNILWQPGRALTGNSVFVQYKIMFSCSMKSSHOKPSCGWQHISCN 89  
||| : ||| : ||| : ||| : ||| : ||| : ||| :  
Db          39 KPANITELSNMKNVLQWTPTPEGLGVKYTVTQYFI----- 75  
:  
QY          90 FPGCRTLAKYGQRQWNKEDCWGTQEUSCDLTSETSDIQEYPYIGRVRAASAGSYSEWSMT 149  
||||:||||:||||:||||:||||:||||:||||:||||:  
Db         76 -----YGKKWLNKSECNRNRTYCDLSAETSDVEHQYAKVAIWGTKCSKWAES 126  
:  
QY        150 PRTPPWETKDIPPMNIQTONGSLLVLHPNLPIRYQCKEKNVSIEDYY-ELLVRVPFIL 208  
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
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[illegible]

Qy 209 NNSLEKEQKVEGAHRAVEIEALTPHSSYCVVAIEIYQPMIDRRSQRSEERC 259
Db 187 NTKSNRTWSQCVNHTLV-LTWLEPNTLYCVHVESFVPGPPRAQPSEKQC 236

RESULT 10
US-08-943-087-24
; Sequence 24, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Fairrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-24

Query Match 21.6%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

Qy 30 KPORVQQRNFHILQWQGRALTGNSSVYFVQYKIMFSCSMKSSHQKPGSCWQHISCN 89
Db 39 KPNATITFLSNKMNVLQWTPPEGLQGVKVTYVQYFI----- 75
Qy 90 FPGCRTLAKYQORWKNKEDCWGTQELSCDLTSETSDIOBPYGRVRAASAGSYSEWSMT 149
Db 76 -----YQCKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIVGTCKSKWAES 126
Qy 150 PRFTPMETKIDPPVMNITQVNGSLLVILHAPNLPYRQKEKNVSIEDYY-ELLYRVFII 208
Db 127 GRFPFLETQIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQIYNLKNYNSVL 186
Qy 209 NNSLEKEQKVEGAHRAVEIEALTPHSSYCVVAIEIYQPMIDRRSQRSEERC 259

Db 187 NTKSNRTWSQCVNHTLV-LTWLEPNTLYCVHVESFVPGPPRAQPSEKQC 236

RESULT 11
US-08-943-087-26
; Sequence 26, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Fairrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-26

Query Match 21.6%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

Qy 30 KPORVQQRNFHILQWQGRALTGNSSVYFVQYKIMFSCSMKSSHQKPGSCWQHISCN 89
Db 39 KPNATITFLSNKMNVLQWTPPEGLQGVKVTYVQYFI----- 75
Qy 90 FPGCRTLAKYQORWKNKEDCWGTQELSCDLTSETSDIOBPYGRVRAASAGSYSEWSMT 149
Db 76 -----YQCKWLKSECRNINRTYCDLSAETSDYEHQYAKVKAIVGTCKSKWAES 126
Qy 150 PRFTPMETKIDPPVMNITQVNGSLLVILHAPNLPYRQKEKNVSIEDYY-ELLYRVFII 208
Db 127 GRFPFLETQIGPPEVALTTDEKSI SVLTAPEKWKNPEDLPVSMQIYNLKNYNSVL 186
Qy 209 NNSLEKEQKVEGAHRAVEIEALTPHSSYCVVAIEIYQPMIDRRSQRSEERC 259
Db 187 NTKSNRTWSQCVNHTLV-LTWLEPNTLYCVHVESFVPGPPRAQPSEKQC 236

RESULT 12

US-08-943-087-28
; Sequence 28, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-943-087-28

Query Match 21.6%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;
QY 30 KPVQVQSRNFHILQWQGRALTGNSVYFVQYKIMFSCSMKSSHQKPGSCWQHISCN 89
Db 39 KPNITFLSINMKNVLQWTPPEGLQGVKVTYVQYFI----- 75
QY 90 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 149
Db 76 -----YGQKWLKSECRNINRYCDLSAETSDYEHQYAKVKAIWGTKCKWAES 126
QY 150 PRTPPWETKIDPPVNNITQVNGSLVILHAPNLPRYQKEKNVSTEDYY-ELLYRVFII 208
Db 127 GRFPFLETQIGPPEVALTTDEKSIISVLTAPKWKRNPEDLFVSMQIYSLNLYNSVL 186
QY 209 NNSLEKEQKVEGAHRAVEIALTPHSSYCVVAEIIYOPMLDRSQRSEERC 259
Db 187 NTKSNRTWSCVCTNHTLV-LTWLEPNTLYCVHVESFVPGPPRAQPSKQC 236

RESULT 13

US-08-943-087-28
; Sequence 28, Application US/08943087

US-08-943-087-30
; Sequence 30, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-943-087-30

Query Match 21.6%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;
QY 30 KPVQVQSRNFHILQWQGRALTGNSVYFVQYKIMFSCSMKSSHQKPGSCWQHISCN 89
Db 39 KPNITFLSINMKNVLQWTPPEGLQGVKVTYVQYFI----- 75
QY 90 FPGCRTLAKYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMT 149
Db 76 -----YGQKWLKSECRNINRYCDLSAETSDYEHQYAKVKAIWGTKCKWAES 126
QY 150 PRTPPWETKIDPPVNNITQVNGSLVILHAPNLPRYQKEKNVSTEDYY-ELLYRVFII 208
Db 127 GRFPFLETQIGPPEVALTTDEKSIISVLTAPKWKRNPEDLFVSMQIYSLNLYNSVL 186
QY 209 NNSLEKEQKVEGAHRAVEIALTPHSSYCVVAEIIYOPMLDRSQRSEERC 259
Db 187 NTKSNRTWSCVCTNHTLV-LTWLEPNTLYCVHVESFVPGPPRAQPSKQC 236

RESULT 14

US-08-943-087-32
; Sequence 32, Application US/08943087

```

; Patent No. 5945511
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-32

```

```

Query Match      21.6%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

Qy 30 KPORVQFSRNFHILQWQGRALTGNSSVYFVQYKIMFSCMSKSHQKPGCQWHISCN 89
Db 39 KPNITFLSINMKNVLQWTPPEGLOGVKVTVTVQYFI----- 75
Qy 90 FPGCRTLAKYQGRQWKNCDCWGTQELSCDITSETSDIQEPYGRVRAASAGSYSEWSMT 149
Db 76 -----YGQKWLNKSECRNIRTYCDLSAETSDYEHQYAKVAKIWTGCKSKWAES 126
Qy 150 PRFTPWETKIDPPVNMITQVNGSLVILHAPNLPRYQKEKNVSIEDIY-ELLYRVFII 208
Db 127 GRFPFLETQIGPPEVALTTDEKISVVLTAPEKWKRPDLPSVMOQIYSLNLYNSVL 186
Qy 209 NNSLEKQKVEYGAHRAVEIEALTPHSSYCVVAEIIYQPMLDLRRSQRSEERC 259
Db 187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPPPPRAQPSSEKQC 236

```

```

RESULT 15
US-08-943-087-34
; Sequence 34, Application US/08943087
; Patent No. 5945511
; GENERAL INFORMATION:

```

```

; APPLICANT: Lok, Si
; APPLICANT: Kho, Choon J.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Farrah, Theresa M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,087
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,305
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-24C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-943-087-34

```

```

Query Match      21.6%; Score 310; DB 2; Length 553;
Best Local Similarity 32.0%; Pred. No. 9.3e-27;
Matches 74; Conservative 33; Mismatches 90; Indels 34; Gaps 3;

Qy 30 KPORVQFSRNFHILQWQGRALTGNSSVYFVQYKIMFSCMSKSHQKPGCQWHISCN 89
Db 39 KPNITFLSINMKNVLQWTPPEGLOGVKVTVTVQYFI----- 75
Qy 90 FPGCRTLAKYQGRQWKNCDCWGTQELSCDITSETSDIQEPYGRVRAASAGSYSEWSMT 149
Db 76 -----YGQKWLNKSECRNIRTYCDLSAETSDYEHQYAKVAKIWTGCKSKWAES 126
Qy 150 PRFTPWETKIDPPVNMITQVNGSLVILHAPNLPRYQKEKNVSIEDIY-ELLYRVFII 208
Db 127 GRFPFLETQIGPPEVALTTDEKISVVLTAPEKWKRPDLPSVMOQIYSLNLYNSVL 186
Qy 209 NNSLEKQKVEYGAHRAVEIEALTPHSSYCVVAEIIYQPMLDLRRSQRSEERC 259
Db 187 NTKSNRTWSQCVTNHTLV-LTWLEPNTLYCVHVESFVPPPPRAQPSSEKQC 236

```

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Search completed: December 12, 2003, 12:16:32
Job time : 26.8542 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 12:23:03 ; Search time 24.0712 Seconds
(without alignments)
1050.732 Million cell updates/sec

Title: US-10-047-264A-4
Perfect score: 1432
Sequence: 1 MNPXCHFLGLISFLTGVA.....YQPMIDRRSQRSERCVIEIP 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description |
|------------|-------|-------|--------|----------|--------------------|
| 1 | 164.5 | 11.5 | 575 | 2 A49667 | interleukin-10 rec |
| 2 | 163 | 11.4 | 295 | 1 KFHU3 | tissue factor prec |
| 3 | 158 | 11.0 | 560 | 2 S27387 | interferon alpha r |
| 4 | 156 | 10.9 | 349 | 2 JC6311 | interferon recepto |
| 5 | 155 | 10.8 | 578 | 2 I56215 | interleukin-10 rec |
| 6 | 149.5 | 10.4 | 325 | 2 A47003 | cytokine receptor |
| 7 | 138.5 | 9.7 | 232 | 1 KFB03 | tissue factor prec |
| 8 | 136.5 | 9.5 | 557 | 2 A32894 | interferon alpha/b |
| 9 | 134.5 | 9.4 | 590 | 2 A45283 | interferon alpha/b |
| 10 | 132.5 | 9.3 | 232 | 1 KFRB3 | tissue factor prec |
| 11 | 122.5 | 8.6 | 489 | 2 A31555 | interferon gamma r |
| 12 | 122 | 8.5 | 294 | 1 KFM33 | tissue factor prec |
| 13 | 110.5 | 7.7 | 332 | 2 A49947 | interferon gamma r |
| 14 | 103.5 | 7.2 | 535 | 2 I39073 | interferon alpha-b |
| 15 | 101.5 | 7.1 | 331 | 2 A54295 | interferon alpha/b |
| 16 | 101.5 | 7.1 | 331 | 2 S59501 | interferon recepto |
| 17 | 92 | 6.4 | 337 | 2 I38500 | interferon gamma r |
| 18 | 90 | 6.3 | 1253 | 1 VHWV | structural polypro |
| 19 | 88 | 6.1 | 755 | 2 S42462 | structural polypro |
| 20 | 87.5 | 6.1 | 674 | 2 A47222 | Kallmann syndrome |
| 21 | 87.5 | 6.1 | 676 | 2 B47222 | Kallmann syndrome |
| 22 | 87 | 6.1 | 1145 | 2 S37136 | structural polypro |
| 23 | 87 | 6.1 | 1384 | 2 T02748 | hypothetical prote |
| 24 | 86 | 6.0 | 477 | 2 A43368 | interferon gamma r |
| 25 | 85 | 5.9 | 792 | 2 S16880 | ribonucleoside-dip |
| 26 | 85 | 5.9 | 810 | 2 E71550 | probable phospholi |
| 27 | 85 | 5.9 | 1059 | 2 T13928 | probable transcrip |
| 28 | 85 | 5.9 | 1083 | 2 T13929 | probable transcrip |
| 29 | 84.5 | 5.9 | 703 | 2 T41065 | RNA binding protei |

gene B9R protein -
hypothetical prote
hemolysin export s
hypothetical prote
sensor protein kin
hypothetical prote
hypothetical prote
calpain IEC 3.4.22
structural polypro
hemolysin secretio
beta-glucosidase h
il-13kappa 1 prot
choline kinase IEC
hypothetical prote
probable exported
hypothetical prote

ALIGNMENTS

RESULT 1
A49667
interleukin-10 receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000
C/Accession: A49667
R/Ho, A.S.; Liu, Y.; Khan, T.A.; Hsu, D.H.; Bazan, J.F.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 11267-11271, 1993
A/Title: A receptor for interleukin 10 is related to interferon receptors.
A/Reference number: A49667; MUID:94068585; PMID:8248239
A/Accession: A49667
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-575 <RES>
A/Cross-references: GB:I12120; NID:G437615; PID:AAA16156.1; PID:G437616
C/Genetics:
A/Gene: IL10r
C/Superfamily: interleukin-10 receptor IL10R
C/Keywords: cytokine receptor

Query Match 11.5%; Score 164.5; DB 2; Length 575;
Best Local Similarity 26.7%; Pred. No. 1.4e-06;
Matches 74; Conservative 37; Mismatches 89; Indels 77; Gaps 16;
QY 7 FLGLISFLTGVA-GTQSTHSLKPRVQFQGRNHNILQWOPGRALTGNSVYFQYK 65
DB 8 FLVTISLSLEFYAGT-ELPSPSYVMFEARFFQHLHWKP--IPNQSESTY---YE 58
QY 66 IMFSCMSKSHQKPSGCWQHISCNPPGCRTLAKYQORQWKNKEDCWGTOLSCDLTSETS 125
DB 59 V-----ALQYGNSTWNDIHCRAQALSCDLITFTL 90
QY 126 DIQEPYVG---RVRAAGSYSEWSMT-PRFTPWETKIDPPVNMITQV-----NGSLLV 176
DB 91 DLYHRSYGYRARRVADNSQYSNWTTTTRFT-----VDEVILTVDSTVLKAMDGIYG 144
QY 177 ILHAPNLPYRQKRNVSIEDYIELLY---RVFIINNSLEKEQKVEGAHRAVEIEALT- 232
DB 145 TIHPP-----RPTITPAGDEYEQVKDLRVYKI--SIRKFSSEL-KNATKRVQKETFTL 194
QY 233 ----PHSSYCVVAEIVQPMIDRR---SQSSEERCVEI 262
DB 195 TVPIGVKFCVKV---LPRLESIRINKAEWSEOCILLI 228

RESULT 2
KFHU3
tissue factor precursor [validated] - human
N/Alternate names: coagulation factor III
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Dec-2000
C/Accession: A43645; A47574; A28320; A29062; A29067; A29068

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QY  71  SMKSSHQKPSGCWQHISCNFPFGCRTLAKYQGRQKNKEDCWGTQELSCDLTSE--TSDIQE 129
Db  71  STKSG-----DKSK--CFYTTDTSCDLTDEIVKDVQK 101

QY  130  PYYGRV-----PAAAGSYSE--WSMTPRFTFWETKI--DPPVMAITGVNGSLVLILHA 180
Db  102  TYLARVFSVPAGNVSTGAGEPLYNSPEFTPYLETLNLGQPTIQSGFEQVGTQKVNVTVED 161

QY  181  PNLFPYRYQKEKNVSIEDYY--ELLYYVFVFINNSLEKEQKYVEGAHR--AVEIALTPHSSY 237
Db  162  ERTLVR--RNTFLSLRDVFGKDLIYLYYKWKSSSGKTKTAKTNTNEFLIDVD---KGENY 217

QY  238  C--VVAEIYQPMLDRRSQSERVCV 260
Db  218  CFSQVQVIPSRTVNRKSTDSPVECM 242

RESULT 3
S27387
interferon alpha receptor type 1 precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S27387; S33770
R;Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
FEBS Lett. 313, 255-259, 1992
A;Title: Specific antiviral activities of the human alpha interferons are deter-
A;Reference number: S27387; MUID:93076908; PMID:1446745
A;Accession: S27387
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-560 <MOU>
A;Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; PID:g432
A;Experimental source: MDBK cells
R;Lim, J.K.; Langer, J.A.
Biochim. Biophys. Acta 1173, 314-319, 1993
A;Title: Cloning and characterization of a bovine alpha interferon receptor.
A;Reference number: S33770; MUID:93305725; PMID:8318540
A;Accession: S33770
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-421,'V' 423-560 <LIM>
A;Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188
A;Experimental source: lung
C;Keywords: antiviral; cytokine receptor; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-560/Product: interferon alpha receptor type 1 #status predicted <MAT>

Query Match 11.0%; Score 150; DB 2; Length 560;
Best Local Similarity 24.1%; Pred. No. 4.9e-06;
Matches 57; Conservative 38; Mismatches 100; Indels 42; Gaps 8;

QY  22  TQSTHSLKPRQVQFSRNFHILQWOPGRALTGNSSVVFQYKIMFSCMKSSHQKPSG 81
Db  223  TTERHKVSPENIQINADNQIYVLKWD---VYENATQADQLRAFFKKIPGNHSD--- 275

QY  82  CQWQHISCNFPFGCRTLAKYQGRQKNKEDCWGTQELSCDLTSETSDIQEYPYGRVRAASAG 141
Db  276  -----KWKQIPNCENVTSTHCVPREVSS--RGIYYVVRASNGN 313

QY  142  SYSEWSMTPRFTFWETKIDPPVMAITGV--NGSLVLILHAPNLVRYQKEKNVSIEDYYE 200
Db  314  GTSFWSSEKEFEFNTENKTIFFPPIVSVKYSTDDSLHVSVCAS-----ESENMSNVQLYP 367

QY  201  LLYRYFINNSLEKEQKYVEGAHRAVEIALTPHSSYCVVAEIYQPML--DRRSQRS 255
Db  368  LIYVIFWENTSNABRKVLKRTNFI--FPDLKPLTVYCVKA---RALIENDRRNKGK 420

RESULT 4
JC6311
interferon receptor-class II cytokine receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

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C;Accession: JC6311
 R;Gibbs, V.C.; Pennica, D.
 Gene 186, 97-101, 1997
 A;Title: CRF2-4: Isolation of cDNA clones encoding the human and mouse proteins.
 A;Reference number: JC6311; MUID: 97193375; PMID: 9047351
 A;Accession: JC6311
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-349 <GIB>
 A;Cross-references: GB:U53696

Query Match 10.8%; Score 156; DB 2; Length 349;
 Best Local Similarity 26.8%; Pred. No. 4e-06;
 Matches 72; Conservative 30; Mismatches 89; Indels 78; Gaps 13;

QY 6 CFFGLISFFLTGAGTQSTHSLKQVQFQSRNFHILQWQ----PGRALTGNSVYF 61
 DB 4 CVAGLGGFLPALGMP-----PPEKRVNVSFNFHILQWVEVPAPFKNL 53
 QY 62 VQKIMFS-----CSMKSHQKSCWQHISCNFPGCRTLAKYQORQWKNKDCWGTQELS 117
 DB 54 AQVESYRSFQDCHKRTASTQ-----CDF-----SHLSKYGD----- 84
 QY 118 CDLTSETSDIQEYGRVRAASAGSYSEWSMTFRFTFWETKIDPPVNNITQVNGSLVI 177
 DB 85 -----YTVRVRRAELADEHSEW-VNVTFCPEVDITIGPPEMQIESLAESLELR 130
 QY 178 LHAPNLPRYQKE-----KNVSIEDYVELLYRV-PIINNSLEKEQKVEGAHRAVEIEA 230
 DB 131 FSAPOI-----ENPFWTLQNI-----YDSWAYRVQYWKNGTNEKFQVV--SPYDSEVLRN 180
 QY 231 LTPHSSYCVVAEIIYQPMPLDRRSORSEERC 259
 DB 181 LEPWTVYCIQVGFLLDQRTGSESEPIC 209

RESULT 5
 156215
 Interleukin-10 receptor - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Jul-2000
 R;Liu, Y.; Wei, S.H.; Ho, A.S.; de Waal Malefyt, R.; Moore, K.W.
 J. Immunol. 152, 1821-1829, 1994
 A;Title: Expression cloning and characterization of a human IL-10 receptor.
 A;Reference number: 156215; MUID: 94165477; PMID: 8120391
 A;Accession: 156215
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-578 <RES>
 A;Cross-references: EMBL:U00672; NID:G482802; PIDN:AAAI7896.1; PID:G482803
 C;Genetics:

Query Match 10.8%; Score 155; DB 2; Length 578;
 Best Local Similarity 22.9%; Pred. No. 9.5e-06;
 Matches 64; Conservative 42; Mismatches 103; Indels 70; Gaps 13;

QY 1 MPEKHFELGLISFFLTGAGTQSTHSLKQVQFQSRNFHILQWQVGRALTGNSVY 60
 DB 1 MLP-CLWVLLAALLSLRLGSDAHGTLPSPSPVWFAEFPHLHWTP----- 47
 QY 61 FVQYKIMFSCKSSHQKSCWQHISCNFPGCRTLAKYQORQWKNKDCWGTQELSCDL 120
 DB 48 -----IPQSESTCYE-----VALLRYGIESWNSISNC--SQTLSYDL 83
 QY 121 TSETSDI--QEPYGRVRAASAGSYSEWSMT-PRFTFWETKIDPPVNNITQV-----NG 172
 DB 84 TAVTLDLYHNGYRARVRAVDGSRHSNWTVTNTRFS-----VDEVTLTVGSVNLHNG 137

QY 173 SLILVILHAPNLPRYQKEKNVSIEDYVELLYRVF-IINNSLEKEQKVEGAHRAVEIEAL 231
 DB 138 FILGKIQLP-----RPMAPANDYISFHSFVEIAIRKVPNGNFTTHKKVKHENF 190
 QY 232 TPHSS-----YCVVAEIIYQPMPLDRRSOR-----SEERCVEI 262
 DB 191 SLTSGEVGFQVQV---KPSVASRSNKGWMSKECISL 226

RESULT 6
 A47003
 cytokine receptor family class II protein CRF2-4 precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 01-Dec-2000
 A;Accession: A47003; G01418
 R;Lutfalla, G.; Gardiner, K.; Uze, G.
 Genomics 16, 366-373, 1993
 A;Title: A new member of the cytokine receptor gene family maps on chromosome 21 at le:
 A;Reference number: A47003; MUID: 93300510; PMID: 8314576
 A;Accession: A47003
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-325 <LUT>
 A;Cross-references: GB:Z17227; NID:G393378; PIDN:CAA78933.1; PID:G393379
 R;Lutfalla, G.
 submitted to the EMBL Data Library, April 1994
 A;Reference number: G06935
 A;Accession: G01418
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-123, 'D', 125-268, 'VGRME' <LU2>
 A;Cross-references: EMBL:U08988; NID:G571295; PID:G571296
 C;Genetics:

Query Match 10.4%; Score 149.5; DB 2; Length 325;
 Best Local Similarity 24.1%; Pred. No. 1.4e-05;
 Matches 57; Conservative 32; Mismatches 89; Indels 59; Gaps 8;

QY 31 PQVQFQSRNFHILQWQVGRALTG-SSVYVQYKIMFSCKSSHQKPSGOWHISC 88
 DB 24 PENRVNVSFNFHILQWSPAFKGLNLTFAQVLSYRIF----- 62
 QY 89 NFPGCRTLAKYQORQWKNKDCWGTQELSCDLTSETSDIQEYVY---RVRAASAGSY 144
 DB 63 -----QDKCMTTLTECDTSSLSK-----YGDHLLVRAEFADHS 98
 QY 145 EWSMTFRFTFWETKIDPPVNNITQVNGSLVILHAPNLPRYQ--KERNVSIEDYVELL 202
 DB 99 DW-VNITFCVDDTIGPPCMQVEVLADSLHMRFLAPKIEYETWTMKNV---YNSWT 153
 QY 203 YRVFIINNSLEKEQKVEGAHRAVEIEALTPHSSYCVVAEIIYQPMPLDRRSORSEERC 259
 DB 154 YNVQYWKNGTDEKFOITPQYDFEV-LRNLEPWTTCVQVRGFLPDRNKAGENSEPVC 209

RESULT 7
 KFB03
 tissue factor precursor - bovine
 N;Alternate names: coagulation factor III
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C;Accession: JQ1319
 R;Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
 Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991
 A;Title: cDNA and amino acid sequences of bovine tissue factor.
 A;Reference number: JQ1319; MUID: 92109720; PMID: 1764065
 A;Accession: JQ1319

A:Molecule type: mRNA
A:Residues: 1-232 <YAK>
A:Cross-references: GB:574147; NID:9241438; PIDN:AAB20755.1; PID:9241439
A:Experimental source: adrenal gland
A>Note: Part of this sequence, including the amino end of the mature protein, was confirmed by the amino acid sequence of the mature protein that serves as a receptor.
C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor for tissue factor. Expression of tissue factor can be induced in a variety of tissues by certain agents.
C:Superfamily: tissue factor
C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane protein
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-292/Product: tissue factor #status experimental <MAT>
F:36-248/Domain: extracellular #status predicted <EXT>
F:249-271/Domain: transmembrane #status predicted <TM>
F:272-292/Domain: intracellular #status predicted <INT>
F:43-153/Binding site: carbohydrate (Aan) (covalent) #status predicted
F:81-89,215-238/Disulfide bonds: #status predicted
F:118,124/Binding site: carbohydrate (thr) (covalent) #status predicted
F:274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 9.7%; Score 138.5; DB 1; Length 292;
Best Local Similarity 22.6%; Pred. No. 0.00011;
Matches 59; Conservative 43; Mismatches 104; Indels 55; Gaps 12;

QY 11 LISFFLTGVAGTQSTHSLKPVQFQSRNHNILQWPGRLATGNSSVYFVQYKMFSC 70
DB 21 LFLGLVLIQAGVAGTDDVVAYNITWKTSTFLEWEPKI---NHVYTVQIS----- 71
QY 71 SMKSHQKSGCGQWHSNCPGRTLAKYQGRQWKNKDCWGTQELSCDLTSE-TSDTQE 129
DB 72 -----PRLG--NWKNK--CFYTTNTECDVTDIIVKNVRE 101
QY 130 PYYGRVRAASAGSYSE-----WSMTPRTPPWETKI-DPPVNNITQVNSGLVILHAPNL 183
DB 102 TVLARVLSTPADTSSSTVPPPTNSPEFTPIYELTNLQGTIOSEFQGVTKLVNTVDART 161
QY 184 PYRYQKEKNVSIEDYY--ELLVYRVTIINNSLSKEQKVYEGARH-AVEIETALPHSSYC-- 238
DB 162 LVR-ANSAFLSLRDVFGDLNLTLYYKASSTGKKATNTNGFLDVID--KGENYCFH 217
QY 239 VVAEYQPMLDRRSRQSEERC 259
DB 218 VQAVILSRVQKSPESPIKC 238

RESULT 8
A:2694
interferon alpha/beta receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 22-Oct-1999
C:Accession: A32694; S17112
R:Uze, G.; Lutfalla, G.; Gresser, I.
Cell 60, 225-234, 1990
A:Title: Genetic transfer of a functional human interferon alpha receptor into mouse cells.
A:Reference number: A32694; MUID:90124632; PMID:2153461
A:Accession: A32694
A:Molecule type: mRNA
A:Residues: 1-557 <UZE>
A:Cross-references: GB:J03171; NID:9184645; PIDN:AAA52730.1; PID:9306914
R:Uze, G.
Submitted to the EMBL Data Library, July 1991
A:Description: The structure of the human interferon alpha/beta receptor gene.
A:Reference number: S17112
A:Accession: S17112
A:Molecule type: DNA
A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>
A:Cross-references: EMBL:X60459; NID:932671
C:Genetics:
A:Gene: GDB:IFNAR1; IFNAR; IFRC
A:Cross-references: GDB:120078; OMIM:107450
A:Map position: 21q22.1-21q22.1
A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
F:1-21/Domain: transmembrane #status predicted <TRN1>

F:437-455/Domain: transmembrane #status predicted <TRN2>
F:50,58,81,88,110,172,254,313,314,376,416,433,507,518,537/Binding site: carbohydrate (

Query Match 9.5%; Score 136.5; DB 2; Length 557;
Best Local Similarity 20.8%; Pred. No. 0.00039;
Matches 54; Conservative 39; Mismatches 115; Indels 51; Gaps 7;

QY 3 PKHCFGLISFFLTGVAGTQSTHSLKPVQFQSRNHNILQWPGRLATGNSSVYFV 62
DB 217 PVHCT-----KTTVENELPPENIEVSQVQNYVLKWD-----YTYANWTFQV 259
QY 63 QYKIMFSCSMKSHQKSGCGWHSNCPGRTLAKYQGRQWKNKDCWGTQELSCDLTSS 122
DB 260 QWLHAFKRNPCNH-----LYKWKQIPDCENVKTTQCVFPQ 295
QY 123 ETSIDQIEPYGRVRAASAGSYSEWSMTPTPTPWETKIDPPVNNITQVNSGLVILHAPN 182
DB 296 NVFQ-KGIYLRVQASDGNNTSFWSSEIKFTDTEQAFLLPPVFNIRSDSPHIYIGAP- 353
QY 183 LPYRYQKEKNVSIEDYYELLVYRVTIINNSLSKEQKVYEGARHRAVEIETALPHSSYCVVAE 242
DB 354 -----KQSGNTFVQDYPYLIYELFWNTSNAERKLIH-KKTDVTVPNLKPLTVYCVKAR 407
QY 243 IY--QPMLDRRSRQSEERC 259
DB 408 AHTMDKLNKSVFSDAVC 426

RESULT 9
A:45283
interferon alpha/beta receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429
R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992
A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homomammalian cells.
A:Reference number: A45283; MUID:92262522; PMID:1533935
A:Accession: A45283
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <UZE>
A:Cross-references: GB:M89641; NID:9194111; PIDN:AAA37890.1; PID:9194112
A>Note: sequence extracted from NCBI backbone (NCBI:102354, NCBI:102357)
R:Lutfalla, G.; Uze, G.
Gene 148, 343-346, 1994
A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-frequency mutation in the extracellular domain.
A:Reference number: I48423; MUID:95047447; PMID:7958966
A:Accession: I48423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 118-125 <RES>
A:Cross-references: EMBL:U06237; NID:9497103; PIDN:AAA65003.1; PID:9755810
A:Accession: I48424
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 127-224 <RE2>
A:Cross-references: EMBL:U06238; NID:9497104; PIDN:AAO1749.1; PID:9755811
A:Accession: I48425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 243-264 <RE3>
A:Cross-references: EMBL:U06239; NID:9497106; PIDN:AAA65004.1; PID:9510261
A:Accession: I48426
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 265-375 <RE4>
A:Cross-references: EMBL:U06240; NID:9497108; PIDN:AAA65005.1; PID:9510262
A:Accession: I48427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 397-424 <RE5>
A:Cross-references: EMBL:U06241; NID:9497110; PIDN:AAA65006.1; PID:9755812

RESULT 12

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Db 8 FLVTISLSLEFIAYGT-----ELPSPSYVWFEPFHILHMKP--IPNQSESTY---YE 58
QY 66 IMFSCSMKSHQKPCSCWOHISCNPFCCRTLAKYQORWKNKEDCWGTQELSCDLTSETFS 125
Db 59 V-----ALQOYGNSTWNDIHCCKAQAQSCDLTTFTL 90
QY 126 DIQEPYVG---RVRAASAGSYSEWSMT-PRFTPMWETKIDPPVMMITQV-----NGSLLV 176
Db 91 DLYHRSYGYRVARVNDVNSQYSNWTTTETFT-----VDEVILTVDSTVKAMGDIY 144
QY 177 ILHAPNLPRYQKKNVSTEDYELLY-----RVFIINNSLEKQKVVYEGHRAHVEIALT- 232
Db 145 TIHP-----RPTITPAGDEYQVFKDLRVYKI--SIRKPSL-KNATKRVKQETFTL 194
QY 233 -----PHSSYCVVARIYQPMLEDR---SQSEERCVET 262
Db 195 TVPIGVKFCVKV-----LPLRESRKINKAWESEQCLLI 228
RESULT 2
TF HUMAN
ID TF HUMAN STANDARD; PRT; 295 AA.
AC P13726;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III)
DE (Thromboplastin) (CD142 antigen).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89247359; PubMed=2719931;
RA Mackman N., Morrissey J.H., Fowler B., Edgington T.S.;
RT "Complete sequence of the human tissue factor gene, a highly
RT regulated cellular receptor that initiates the coagulation protease
RT cascade.";
RL Biochemistry 28:1755-1762(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260946; PubMed=3037536;
RA Spicer E.K., Horion R., Bloem L., Bach R., Williams K.R., Guha A.,
RA Kraus J., Lin T.C., Nemerson Y., Konigsberg W.H.;
RT "Isolation of cDNA clones coding for human tissue factor: primary
RT structure of the protein and cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87244317; PubMed=3297348;
RA Morrissey J.H., Fakhrai H., Edgington T.S.;
RT "Molecular cloning of the cDNA for tissue factor, the cellular
RT receptor for the initiation of the coagulation protease cascade.";
RL Cell 50:129-135(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88050796; PubMed=2823875;
RA Scarpatti E.M., Wen D., Broze G.J. Jr., Miletich J.P.,
RA Flandermeyer R.R., Siegel N.R., Sadler J.E.;
RT "Human tissue factor: cDNA sequence and chromosome localization of
RT the gene.";
RL Biochemistry 26:5234-5238(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=88100453; PubMed=3424286;
RA Fisher K.L., Gorman C.M., Vohar G.A., O'Brien D.P., Lawn R.M.;
RT "Cloning and expression of human tissue factor cDNA.";
RL Thromb. Res. 48:89-99(1987).
RN [6]
RP SEQUENCE FROM N.A., AND VARIANTS ALA-36 AND VAL-145.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,

RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Collier R.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP DISULFIDE BONDS, AND PALMITOYLATION.
RX MEDLINE=8900604; PubMed=3166978;
RA Bach R., Konigsberg W.H., Nemerson Y.;
RT "Human tissue factor contains thioester-linked palmitate and stearate
RT on the cytoplasmic half-cysteine.";
RL Biochemistry 27:4227-4231(1988).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 33-243.
RX MEDLINE=94368785; PubMed=8086403;
RA Muller Y.A., Ultsch M.H., Kelley R.F., de Vos A.M.;
RT "Structure of the extracellular domain of human tissue factor:
RT location of the factor VIIa binding site.";
RL Biochemistry 33:10864-10870(1994).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 33-243.
RX MEDLINE=96190957; PubMed=8609606;
RA Muller Y.A., Ultsch M.H., de Vos A.M.;
RT "The crystal structure of the extracellular domain of human tissue
RT factor refined to 1.7-A resolution.";
RL J. Mol. Biol. 256:144-159(1996).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-251 IN COMPLEX WITH FVIIA.
RX MEDLINE=96175641; PubMed=8598903;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RL Nature 380:41-46(1996).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 37-242 IN COMPLEX WITH FVIIA.
RX MEDLINE=99126538; PubMed=9925787;
RA Zhang E., St Charles R., Tulinsky A.;
RT "Structure of extracellular tissue factor complexed with factor VIIa
RT inhibited with a BPTI mutant.";
RL J. Mol. Biol. 285:2089-2104(1999).
CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- INDUCTION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF

CC CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1
CC AND TNF, AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND
CC VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE
CC RESPONSE.
CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
CC -1- DATABASE: NAMS=PROW; NOTE=CD guide CD142 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd142.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J02931; AAA61150.1; -
CC EMBL; M16553; AAA61151.1; -
CC EMBL; J02846; AAA61152.1; -
CC EMBL; M27436; AAA61153.1; -
CC EMBL; A19048; CAA01438.1; -
CC EMBL; AF540377; AAN01236.1; -
CC EMBL; AL138758; CAC15961.1; -
CC EMBL; BC011029; AAH11029.1; -
CC PIR; A43645; KFHU3.
CC PDB; 1BOV; 10-JUN-96.
CC PDB; 2HT; 29-JAN-96.
CC PDB; 1DAN; 04-SEP-97.
CC PDB; 1AHW; 19-AUG-98.
CC PDB; 1TFH; 19-AUG-98.
CC PDB; 1FAK; 03-DEC-99.
CC PDB; 1JPS; 18-DEC-02.
CC Genew; HGNC:3541; F3.
CC MTM; 134390.
CC GO; GO:0016021; C:integral to membrane; TAS.
CC GO; GO:0003801; F:blood coagulation factor activity; TAS.
CC InterPro; IPR000282; Cytok receptor_2.
CC Pfam; PR01108; Tissue fac; 1.
CC PRINTS; PR00346; TISSUEFACTOR.
CC PROSITE; PS00621; TISSUE FACTOR; 1.
CC Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW Palmitate; 3D-structure; Polymorphism.
FT SIGNAL 1 32
FT CHAIN 33 295
FT DOMAIN 33 251
FT TRANSMEM 252 274
FT SITE 46 48
FT SITE 77 79
FT SITE 190 192
FT CARBOHYD 156 156
FT CARBOHYD 169 169
FT DISULFID 81 89
FT DISULFID 218 241
FT LIPID 277 277
FT VARIANT 36 36
FT VARIANT 145 145
FT VARIANT 163 163
FT CONFLICT 260 260
FT STRAND 42 49
FT TURN 50 51
FT STRAND 52 58
FT STRAND 64 72
FT TURN 73 74
FT STRAND 78 84
FT STRAND 88 90
FT HELIX 92 95
FT HELIX 96 98
FT TURN 99 100

FT STRAND 103 111
FT STRAND 126 128
Query Match 11.4%; Score 163; DB 1; Length 295;
Best Local Similarity 23.4%; Pred. No. 8.2e-08; Gaps 13;
Matches 62; Conservative 45; Mismatches 100; Indels 58;
QY 11 LISFFITGVAGTQSTHESLKQVQFQSRNFHNLQWQGRALTGNSSVYFVQYKIMFSC 70
Db 21 LLGWVPAQVAGASGTTNTVAAYNLTKWSTNFKTILEWPKPV---NQVITVQ-----I 70
QY 71 SMKSHQKSGGCWQHISCNPPGCGRTLAKYGQRQWKNKEDCWGQELSCDLTSE-TSIOE 129
Db 71 STKSG-----DWKSK--CFYTTDTECDLTDEIVKDVQK 101
QY 130 PYYGRV-----RAASAGSYSE--WSMTPRFTPWETKI-DPPVMNITQVNGSLVLHA 180
Db 102 TYLARVFSYPAGNVSTGSGAGEPLYENSPEFTYLETNLGQPTIQSFEQGTKNVTVED 161
QY 181 PNLPRYQKEKNVSIEDYY--ELLYRVFIINNSLEKEQKYVEGAHR-AVEIEALTPHSSY 237
Db 162 ERTLVR-RNNTFLSLRDVFGKLIYLYYWKSSSGKTKTAKTNEFLIDVD---KGENY 217
QY 238 C--VVAEIIQPMPLDRSQSRSEECV 260
Db 218 CFSVQAVIPSRVTWRKSTDSPEVCM 242
RESULT 3
INR1_BOVIN STANDARD; PRT; 560 AA.
ID AC Q04790;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
GN IFNAR1 OR IFNAR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=93076908; PubMed=1446745;
RA Mouchel-Viehl E., Lutfalla G., Mogensen K.E., Uze G.;
RT "Specific antiviral activities of the human alpha interferons are
determined at the level of receptor (IFNAR) structure.";
RL PDBS Lett. 313:255-259 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93305725; PubMed=8318540;
RA Lim J.-K., Langer J.A.;
RT "Cloning and characterization of a bovine alpha interferon receptor.";
RL Biochim. Biophys. Acta 1173:314-319 (1993)
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
CC EMBL; X68443; CAA48484.1; -

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DR EMBL; L06320; AAA02571.1; -.
DR PIR; S27387; S27387.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF01108; Tissue_fac; 1.
DR SMART; SM00060; FN3; 2.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 560
FT DOMAIN 25 437
FT TRANSMEM 438 560
FT DOMAIN 459 560
FT DISULFID 76 84
FT DISULFID 199 220
FT CARBOHYD 47 47
FT CARBOHYD 55 55
FT CARBOHYD 85 85
FT CARBOHYD 109 109
FT CARBOHYD 172 172
FT CARBOHYD 254 254
FT CARBOHYD 313 313
FT CARBOHYD 377 377
FT CARBOHYD 434 434
FT CONFLICT 422 422
SQ SEQUENCE 560 AA; 63818 MW; 66D76B72861BD11 CRC64;

Query Match 11.0%; Score 158; DB 1; Length 560;
Best Local Similarity 24.1%; Pred. NO. 5.3e-07;
Matches 57; Conservative 38; Mismatches 100; Indels 42; Gaps 8;

Qy 22 TQSTHESLKQVQFSNPHNIIQWPGQALTGNSVYFVQYKIMFSCMKSSHQKPSG 81
Db 223 TTERHKVSPENIQINADNQIYLVKWD---YPENATFQAWLRAFFKIPGNHSD--- 275

Qy 82 CWOHISCNFPGCRITLAKYQGRQWKNKDCWGTQELSCLDTSETSDIQPYGYGRVRAASAG 141
Db 276 -----KWQIPNCENVVTHCVFPREVSVS-RGIYVYVRAASNGN 313

Qy 142 SYSWMTPTPTPWETKIDPPVNMITQV-NGSLVLVLHAPNLPYRYQKKNVSDIYDE 200
Db 314 GTSFWSBEKEFTENKTIIFPPVISVSKSVTDDSLHVSVGAS-----ESENMSVNLQYP 367

Qy 201 LLYRVFINNSLEKEQKYEAGHRAVEIEALTPTSSYCVVAEIVQPMI--DRRSQRS 255
Db 368 LIYEVIFWNTSNAERKYLEKRTNFI-FPDLKPLTVYCVKA---RALIENDRRNKG 420

RESULT 4
ID IL10_MOUSE STANDARD; PRT; 349 AA.
AC Q61190;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
DE (Cytokine receptor class-II CRF2-4).
GN IL10R OR CRFB4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9719375; PubMed=9047351;
RA Gibbs V.C., Pennica D.;
RT "CRF2-4: isolation of cDNA clones encoding the human and mouse
RL proteins.";
RN Gene 186:97-101 (1997).
RX [2]
RX CHARACTERIZATION.
RX MEDLINE=98130620; PubMed=9463407;

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RA Spencer S.D., Di Marco F., Hooley J., Pitts-Meek S., Bauer M.,
RA Ryan A.M., Sordat B., Gibbs V.C., Aguet M.;
RT "The orphan receptor CRF2-4 is an essential subunit of the interleukin
RL 10 receptor.";
CC J. Exp. Med. 187:571-578 (1998).
CC - FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY
CC CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO
CC INITIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - SIMILARITY: Contains 2 fibronectin type III domains.
CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC -----
CC EMBL; U53696; AAC53062.1; -.
CC MCD; MG1108380; I110rb.
CC GO; GO:0004920; F:interleukin-10 receptor activity; IMP.
CC GO; GO:0005515; F:protein binding activity; IPI.
CC InterPro; IPR000282; Cytok_receptor_2.
CC InterPro; IPR003961; FN_III.
CC SMART; SM00060; FN3; 2.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 349
FT DOMAIN 20 220
FT TRANSMEM 221 241
FT DOMAIN 242 349
FT DOMAIN 113 205
FT DISULFID 66 74
FT DISULFID 188 209
FT CARBOHYD 49 49
FT CARBOHYD 102 102
FT CARBOHYD 161 161
FT CARBOHYD 199 199
SQ SEQUENCE 349 AA; 39774 MW; 58BA4F6B86330A39 CRC64;

Query Match 10.9%; Score 156; DB 1; Length 349;
Best Local Similarity 26.8%; Pred. NO. 4.5e-07;
Matches 77; Conservative 30; Mismatches 89; Indels 78; Gaps 13;

Qy 6 CFFGLISFLTGVAGTQSTHESLKQVQFSNPHNIIQWPGQALTGNSVYFVQYKIMFSCMKSSHQKPSG 61
Db 4 CVAGWLGGLLVPALGMIP-----PPEKVRMNSVNFKNILQWVEVPAPKTNLT-----FT 53

Qy 62 VOYKIMFS-----CSMKSSHQKPSGCGWQHISCNFPGCRITLAKYQGRQWKNKDCWGTQELS 117
Db 54 AQYESYRSFQDHCCKRTASTQ-----CDP---SHLSKYGD----- 84

Qy 118 CDLTSETSDIQPYGYGRVRAASAGSYSEWSMTPTPTPWETKIDPPVNMITQVANGSLVLI 177
Db 85 -----YTVRVRAELADHSEW-VNVTFCPVEDTIIGPPEQIESLAESLHLR 130

Qy 178 LHAPNLPYRYQK-----KNVSDIYDEYELLRYV-FIINNSLEKEQKYEAGHRAVEIEA 230
Db 131 FSAPQI-----ENEPETWTLKNI-----YDSWAYRVQYWKNGTNEKFFQV--SPYDSEVLRN 180

Qy 231 LTHSSYCVVAEIVQPMIDRRSQRSBERC 259
Db 181 LEPWTTYCIQVQGLLQDQRTGEWSEPIC 209

RESULT 5
ID IL10R_HUMAN STANDARD; PRT; 578 AA.
AC Q13651;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Interleukin-10 receptor alpha chain precursor (IL-10R-A) (IL-10R1).
GN IL10RA OR IL10R.
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoma;
RX MEDLINE=94165477; PubMed=8120391;
RA Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;
RT "Expression cloning and characterization of a human IL-10 receptor.";
RL J. Immunol. 152:1821-1829(1994).
CC -|- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- TISSUE SPECIFICITY: SPLEEN, THYMUS, AND BMSC. PAINT EXPRESSION
CC IN PANCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENTA,
CC LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS,
CC LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRESS HIGH LEVELS OF IL-
CC 10R.
CC -|- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
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CC
CC -----
DR EMBL; U00672; AAA17896.1; -.
DR PIR; I56215; I56215.
DR PDB; 1J7V; 19-SEP-01.
DR PDB; 1LQS; 17-JUL-02.
DR Genew; HGNC:5964; IL10RA.
DR MIM; 146933; -.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004920; F:interleukin-10 receptor activity; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR000282; Cytok receptor; 2.
KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 578 INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.
FT DOMAIN 22 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 257 578 CYTOPLASMIC (POTENTIAL).
FT DISULFID 202 223 POTENTIAL.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 578 AA; 62903 MW; EE1B29064338157C CRC64;
Query Match 10.8%; Score 155; DB 1; Length 578;
Best Local Similarity 22.9%; Pred. No. 1e-06;
Matches 64; Conservative 42; Mismatches 103; Indels 70; Gaps 13;
QY 1 MNPKEFLGLFLTGVAGTQSTHSLKPRQVQFSRNFNFIQWQGRALTGNSSVY 60
DB 1 MLP-CLVLLAALLSLRGLSDAHGTSLPSPVWFEEAFFHILHWTP----- 47
QY 61 FVOYKIMFSCMKSHQKSGCQWHISCNPPGCRITLAKYQGRQWKNKBCWGTQELSCDL 120
DB 48 -----IPQSESTCYE-----VALLRYGIESWNSISNC--SQTLSYDL 83
QY 121 TSETSDI--QEPYGVRAASAGSISEWSMT-PRFTPWETKIDPPVMNITQV-----NG 172
DB 84 TAVTLDLHNSGVRAVRVADGSRHSNVTVTNTRFS-----VDEVTLTVGVSINLEIHHG 137
QY 173 SLVLVILHAPNLPYRKQKVNSTEDYELLYRVF-IINNSLEKEQKVEGAHRAVEIAL 231

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DB 138 FILGKQLP-----RPMQVANDYISIFSHFREYETAIKRVGNFTTHKKVKNHF 190
QY 232 TPHSS-----YCVVAIIYQPMIDRRSQR---SEERCVEI 262
DB 191 SLTTSGEVGFQVQV---KPSVASRSNKGWMSKECISL 226
RESULT 6
ID 110S_HUMAN STANDARD; PRT; 325 AA.
AC Q08334;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
DE (CYTOKINE RECEPTOR CLASS-II CRF2-4).
GN IL10RB OR CRFB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=93300510; PubMed=8314576;
RA Lutfalla G., Gardiner K., Uze G.;
RT "A new member of the cytokine receptor gene family maps on chromosome
RT 21 at less than 35 kb from IFNAR.1";
RL Genomics 16:366-373(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96054036; PubMed=7563119;
RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT "Structure of the human CRFB4 gene: comparison with its IFNAR
RT neighbor.";
RL J. Mol. Evol. 41:338-344(1995).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=97459974; PubMed=9312047;
RA Kotenko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,
RA Pestka S.;
RT "Identification and functional characterization of a second chain of
RT the interleukin-10 receptor complex.";
RL EMBO J. 16:5894-5903(1997).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=20469498; PubMed=10875937;
RA Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,
RA Wood W.I., Goddard A.D., Gurney A.L.;
RT "Interleukin (IL)-22, a novel human cytokine that signals through the
RT interferon receptor-related proteins CRF2-4 and IL-22R.1";
RL J. Biol. Chem. 275:31335-31339(2000).
CC -|- FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY
CC CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO
CC INITIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- SIMILARITY: Contains 2 fibronectin type III domains.
CC -|- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
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CC
CC -----
DB EMBL; Z17227; CAA78933.1; -.
DR EMBL; U08988; AAA86872.1; -.
DR PIR; A47003; A47003.
DR HSSP; P13726; 1TFH.
DR Genew; HGNC:5965; IL10RB.

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Okabayashi Y., Muta T., Miyata T., Iwanaga S.;
CDNA and amino acid sequences of bovine tissue factor.";
Biochem. Biophys. Res. Commun. 181:1145-1150(1991).


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FT DOMAIN 28 436 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 437 457 CYTOSOLIC.
FT DOMAIN 458 557 CYTOPLASMIC (POTENTIAL).
FT DISULFID 79 87 BY SIMILARITY.
FT DISULFID 199 220 PHOSPHORYLATION (BY TYK2) (PROBABLE).
FT MOD RES 466 481 PHOSPHORYLATION (BY TYK2) (PROBABLE).
FT MOD RES 481 481 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 254 254 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 376 376 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 416 416 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 433 433 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 168 168 L -> V.
FT CONFLICT 17 17 /FTid=VAR_002717.
FT SEQUENCE 557 AA; 63525 MW; 0F6744C8A1ADBE73 CRC64;

Query Match 9.5%; Score 136.5; DB 1; Length 557;
Best Local Similarity 20.8%; Pred. No. 5.3e-05;
Matches 54; Conservative 39; Mismatches 115; Indels 51; Gaps 7;

Qy 3 PKHCPGLGFLISFLLTGAGTSTHSLKPQVQFOSRNFHILQWPGRALTGNSVVFV 62
Db 217 PVHCI-----KTTVENLPPPEINIEVSQNVYLVKWD-----YTYANMTFQV 259
Qy 63 QYKMFCSMKSSHQKPSGCGWHISCNFPFCRTLAKYQORWKNKEDCWGTQELSCDLS 122
Db 260 QWLHAFKRNPGNH-----LYKWQIPDCENKTTQCVFPQ 295
Qy 123 ETSIDQIEPYGRVRAASAGSYSEWSMTPTFTPWETKIDPPVMNITQVNGSLVILHAPN 182
Db 296 NVFO-KGIYLRVQASDGNWTSFWSSEIKFTETQAFLLPPVFNIRSLDSFHIYIGNP- 353
Qy 183 LPYRYQKEKNVSIEDYBELLRVFPIINSLKEQKVEGAHRAVEIEALTPHSYCVVAE 242
Db 354 ----KQSGNTPVQDYPLVEIIPWENTSNAERKIE-KKTDVTPNKLPLTVYCVKAR 407
Qy 243 IY-QPMLDRSQRSEERC 259
Db 408 AHTWDEKLNKSVFSFSDAYC 426

RESULT 10
ID INRI_SHEEP STANDARD; PRT; 560 AA.
AC Q28589; Q95206;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE (interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC)
GN (interferon alpha/beta receptor-1).
OS IFNARI OR IFNAR.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RX MEDLINE=97135690; PubMed=8981227;
RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick B.L., Flint A.P.F.;
RT "Structure of an ovine interferon receptor and its expression in
RL endometrium."
RN J. Mol. Endocrinol. 17:207-215(1996).
RN [2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium;
RX MEDLINE=98006426; PubMed=9348203;
RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;
RT "Molecular cloning of ovine and bovine type I interferon receptor
RT subunits from uteri, and endometrial expression of messenger
RT ribonucleic acid for ovine receptors during the estrous cycle and
RT pregnancy."
RL Endocrinology 138:4757-4767(1997).
CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
CC SUBUNITS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT
CC CONCEPTUS AT DAY 15 OF PREGNANCY.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X95939; CAA65183.1; --
CC EMBL; U65978; AAB84231.1; --
CC InterPro; IPR000282; Cytok receptor_2.
CC InterPro; IPR003961; FN_III.
CC SMART; SM00060; FN3_2.
CC Receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 24 BY SIMILARITY.
CC CHAIN 25 560 INTERFERON-ALPHA/BETA RECEPTOR ALPHA
CC CHAIN.
CC DOMAIN 25 437 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 438 458 POTENTIAL.
CC DOMAIN 459 560 CYTOPLASMIC (POTENTIAL).
CC DISULFID 76 84 BY SIMILARITY.
CC DISULFID 199 220 BY SIMILARITY.
CC CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 55 55 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 108 108 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 222 222 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 359 359 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 377 377 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 434 434 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CONFLICT 352 522 S -> G (IN REF. 2).
CC CONFLICT 522 522 A -> D (IN REF. 2).
CC SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;

Query Match 9.5%; Score 136.5; DB 1; Length 560;
Best Local Similarity 23.3%; Pred. No. 5.3e-05;
Matches 57; Conservative 32; Mismatches 109; Indels 47; Gaps 8;

Qy 22 TQSTHSLKPQVQFOSRNFHILQWPGRALTGNSVVFQYKMFCSMKSSHQKPSG 81
Db 223 TTERHKVPSPEINQVNDVNOAYVLKWD-----YPYESTTFOAQLRAFLKPIGKH----- 273
Qy 82 CWOHISCNFPFCRTLAKYQORWKNKEDCWGTQELSC-----DLTSETSDIQEYIGVRA 137
Db 274 -----SNKWKQIPNCENVITTHCVFPRDIFS-----MGIYVVRVA 309
Qy 138 ASAGSYSEWSMTPTFTPWETKIDPPVMNITQV-NGSLVILHAPNLPYRYQKEKNVSI 196
Db 310 SNGNGTSFWSEEKFEFTEVPKPIFPFVISMKSITDSDLHVSVAS-----EESNMSVN 363

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QY 197 DYELLYRVFIINNSLEKQKVEGAHRAVEIALTHSSYCVVAE--IYQPMLEDRRSOR 254
 Db 364 QLYPLVYEVIFWENTNAERKVLK-KRTDFTPNLKLPLVYCVKARALIENDRWNGSSY 422
 QY 255 SEERC 259
 Db 423 SDTVC 427

RESULT 11
 INR1 MOUSE
 ID INR1 MOUSE STANDARD; PRT; 590 AA.
 AC P3396;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Interferon-alpha/beta receptor alpha chain precursor (IFN-alpha-REC).
 GN IFNARI OR IFNAR OR IFAR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=92262522; PubMed=1533935;
 RX Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;
 RA "Behavior of a cloned murine interferon alpha/beta receptor expressed
 RT in homoeopisic or heterospecific background";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).
 CC -!- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
 CC SUBUNITS THEMSELVES.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
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 CC
 CC EMBL; M89641; AAA37890.1; -;
 DR PIR; A45283; A45283.
 DR MGD; MGI:107658; Ifnar1.
 DR InterPro; IPR000282; Cytok receptor_2.
 DR InterPro; IPR003961; FN_III.
 DR SMART; SM00060; FN3; 3.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 590
 FT INTERFERON-ALPHA/BETA RECEPTOR ALPHA
 FT CHAIN.
 FT DOMAIN 27 429
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 430 449
 FT POTENTIAL.
 FT DOMAIN 450 590
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 78 96
 FT BY SIMILARITY.
 FT DISULFID 199 220
 FT BY SIMILARITY.
 FT CARBOHYD 43 43
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 109 109
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 181 181
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 214 214
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 314 314
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 370 370
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 409 409
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 413 413
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 590 AA; 65776 MW; 7EC6DFP370185D3A CRC64;

Query Match 9.4%; Score 134.5; DB 1; Length 590;
 Best Local Similarity 21.4%; Pred. No. 8.7e-05;
 Matches 45; Conservative 39; Mismatches 99; Indels 27; Gaps 7;

QY 56 NSSVYFV--QYKIMFSCMKSHOKPSCWOHISCNFPGCRTLAKY---GOROWKNKEDC 110
 Db 34 NIDVYIIDNTYTLK-----SSHGSMG-----SVTF-----AEYRTDEAKLKVPEC 78
 QY 111 WGTQELSCDLTSETSDIOEPYVYGRVRAASAGSYSEWSMTPTPTMWTETKIDPPVMMITQV 170
 Db 79 QHTTTTKCFSLDDTNVYIKTQFRVRABEGNSTSSWNEVDPIFPYTAHMSPPVEALEAE 138
 QY 171 NGSLLAVILHAPNLPYRQKKNVSTEDYVELLYRVFIINNSLEKQKVEGAHRAVEIAE 230
 Db 139 DKAILLVHISPPG-----QDGNMWALEKPSFYSYTIWOKS--SSDKKTINSTIYVEKIPE 191
 QY 231 LTPHSSYCVVAEIQPMLDRRSQRSEERC 260
 Db 192 LLPETTYCLEVKAIHPSLKHSNYSTVQCI 221

RESULT 12
 TF RABIT
 ID TF RABIT STANDARD; PRT; 292 AA.
 AC P24055;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tissue factor precursor (Tf) (Coagulation factor III).
 GN F3.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]_SEQUENCE FROM N.A.
 RP TISSUE-Heart;
 RC TISSUE-Heart;
 RX MEDLINE=91200676; PubMed=1840552;
 RA Andrews B.S., Rehemkulla A., Fowler B.J., Edgington T.S., Mackman N.;
 RT "Conservation of tissue factor primary sequence among three mammalian
 RT species";
 RL Gene 98:265-269(1991).
 RN [2]
 CC SEQUENCE OF 33-292 FROM N.A.
 RP STRAIN-New Zealand white; TISSUE-Brain;
 RX MEDLINE=92081032; PubMed=1746002;
 RA Pawashe A., Ezekowitz M., Lin T.C., Horton R., Bach R., Konigsberg W.;
 RT "Molecular cloning, characterization and expression of cDNA for
 RT rabbit brain tissue factor";
 RL Thromb. Haemost. 66:315-320(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 36-240.
 RX MEDLINE=98266351; PubMed=9605315;
 RA Muller Y.A., Kelley R.F., de Vos A.M.;
 RT "Hinge bending within the cytokine receptor superfamily revealed by
 RT the 2.4 A crystal structure of the extracellular domain of rabbit
 RT tissue factor";
 RL Protein Sci. 7:1106-1115(1998).
 CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF.VIIA] COMPLEX ACTIVATES
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROLYSIS. TF PLAYS A ROLE IN
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: BRAIN, HEART.
 CC -!- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
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 CC
 CC EMBL; M55390; AAA63469.1; -;

```
DR EMBL; X53521; CAA37597.1; --
DR PIR; J00441; KFRB3
DR PUB; LA21; 27-MAY-98.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR001187; Tissue_factor_1.
DR Pfam; PF01108; Tissue_fac; 1.
DR PRINTS; PR00346; TISSUEFACTOR.
DR PROSITE; PS00621; TISSUE_FACTOR; 1.
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW Palmitate; 3D-structure.
FT SIGNAL 1 32
FT CHAIN 33 292
FT DOMAIN 33 250
FT TRANSMEM 251 271
FT DOMAIN 272 292
FT SITE 44 46
FT SITE 75 77
FT CARBOHYD 41 41
FT CARBOHYD 114 114
FT CARBOHYD 154 154
FT CARBOHYD 167 167
FT CARBOHYD 182 182
FT DISULFID 79 87
FT LIPID 216 239
FT LIPID 274 274
FT STRAND 40 47
FT TURN 48 49
FT STRAND 50 56
FT STRAND 62 69
FT STRAND 76 82
FT STRAND 86 88
FT HELIX 90 93
FT TURN 94 95
FT TURN 97 98
FT STRAND 101 109
FT STRAND 126 126
FT STRAND 130 130
FT HELIX 132 135
FT STRAND 137 137
FT STRAND 143 149
FT TURN 150 151
FT STRAND 152 157
FT STRAND 161 165
FT STRAND 170 172
FT HELIX 173 177
FT HELIX 178 180
FT STRAND 182 188
FT STRAND 196 200
FT STRAND 204 208
FT TURN 211 212
FT STRAND 216 222
FT TURN 224 225
FT STRAND 231 231
FT STRAND 238 239
SQ SEQUENCE 232 AA; 32738 MW; 4860AICADBACC71 CRC64;

Query Match 9.3%; Score 132.5; DB 1; Length 292;
Best Local Similarity 22.2%; Pred. No. 5.6e-05;
Matches 62; Conservative 39; Mismatches 89; Indels 89; Gaps 13;

QY 11 LISFLLTGVAQTQTHSLKQRFQFQSRNPHNLOWOPGRALGNSVYFVQYKMFSC 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 21 LLGWLAAQVAAADT--TGRAYNLTWSTNFKTILEMEP-----KSIDHV-YTVQIST 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 71 SMKSHQKPCSCQWQHISCNFPCCRTAKYQGRQWKNKDCWGTQELSCDLTSE-TSDIQE 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 71 RLEN-----WSK--CFLTAETECDLTDEVVVKDVGQ 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 130 PYYGRV-----RAASAGSYSE---WSMTPTPTPMWETKIDPPV-----NNITQVN 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 100 TYMARVLSYPARGNTTGFPEPPRNSPFTFYLDNLGQPTIQSPQVGTKLNVTVQD 159
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 GSLVLILHAPNLPYR--YQKKNVSIIEYVELLY-----RVFIINNSLEKQKYEGA 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Db 160 ARTLVRRNGTFLSLRAVFGKDLN-----YLYYWRASSGKKTKATTNTNEFLIDVDKGE 213
QY 223 HRAVEIEALTPHSSYCVVAEIQPMLDRRSQSRSEECVE 261
Db 214 NYCFSVQAVIPSR-----KKRQSPESLUTE 238

RESULT 13
TF_RAT
ID TF_RAT STANDARD; PRT; 295 AA.
AC P42533;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III).
DE CF3.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97108126; PubMed=8950776;
RA Taby O., Rosenfield C.L., Bogdanov V., Nemerson Y., Taubman M.B.;
RT "Cloning of the rat tissue factor cDNA and promoter: identification
   of a serum-response region.";
RL Thromb. Haemost. 76:697-702(1996).
CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
   CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES
   FACTORS IX OR X BY SPECIFIC LIMITED PROLYSIS. TF PLAYS A ROLE IN
   NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
   PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
CC
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   or send an email to license@isb-sib.ch).
CC
CC EMBL; U07619; AAA16966.1; --
CC HSPB; P13726; IFAK.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR001187; Tissue_factor.
DR Pfam; PF01108; Tissue_fac; 1.
DR PRINTS; PR00346; TISSUEFACTOR.
DR PROSITE; PS00621; TISSUE_FACTOR; 1.
KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
KW Palmitate.
FT SIGNAL 1 28
FT CHAIN 29 295
FT DOMAIN 29 252
FT TRANSMEM 253 275
FT DOMAIN 276 295
FT SITE 246 248
FT SITE 38 38
FT CARBOHYD 58 58
FT CARBOHYD 95 95
FT CARBOHYD 109 109
FT CARBOHYD 170 170
FT CARBOHYD 201 201
FT DISULFID 76 84
FT DISULFID 219 242
FT LIPID 276 276
SQ SEQUENCE 295 AA; 33443 MW; E54C15B4E3628D48 CRC64;

Query Match 9.0%; Score 128.5; DB 1; Length 295;
Best Local Similarity 22.9%; Pred. No. 0.00013;
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| DR | InterPro; IPRO00282; Cytok_receptor_2. |
| DR | InterPro; IPRO01187; Tissue_factor. |
| DR | Pfam; PF01108; Tissue_fac.1. |
| DR | PRINTS; PR00346; TISSUEFACTOR. |
| DR | PROSITE; PS00621; TISSUE_FACTOR.1. |
| KW | Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein; |
| KW | Palmitate. |
| FT | SIGNAL |
| FT | CHAIN |
| FT | DOMAIN |
| FT | TRANSNEM |
| FT | DOMAIN |
| FT | SITE |
| FT | CARBOHYD |
| FT | CARBOHYD |
| FT | CARBOHYD |
| FT | CARBOHYD |
| FT | DISULFID |
| FT | DISULFID |
| FT | LIPID |
| FT | CONFLICT |
| SQ | SEQUENCE |

Query Match 8.7%; Score 124; DB 1; Length 294;
 Best Local Similarity 22.7%; Pred.No. 0.00035;
 Matches 64; Conservative 36; Mismatches 100; Indels 82; Gaps 13

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| QY | 7 FLGFLISFFLTGVAGTQSTHESLKPORVQPSQRNFHNILQWPGCRALTGNSSVFVQYKI 66 : : |
| DB | 17 FLGCLLLQVIAG-AGIPE-----KAFNLTWISTDFKILEWQP----KPINYYTYTVQ--- 63 : : |
| QY | 67 MFSCSKSHSQSPSGCWQHISCNPFGCRTLAKYGQRQWKEDCGWGTOELSCDLTSE--TS 125 : : |
| DB | 64 ---ISDRS-----RWNQNK--CFSTDTDECDLTDIEVK 91 : : |
| QY | 126 DTQEPYGYRVRAASA-----GSYSEWSMTPTFPWWETKIDPPV----- 164 : : : : : : : |
| DB | 92 DVTWAYEAKVLSPVRNSVHGDDQLVIHGEPPFTNAKPLPYRDNLQGQPVIOQFEQD 151 : : : : : : : |
| QY | 165 ---MNTQVNGSLLVILHAPNLPRYQKEKNVSIEDYELLRYRVFINNSLEKEQKVVEG 221 : : : : : : : |
| DB | 152 GRKLNVVVKDLSLTVRKNGTFLLRLQVFGKDLG-----YITYRK---GSSTGKKTNITNT 204 : : : : : : : |
| QY | 222 AHRVAERIALTPHSYC--VVAEIYQPMLDRRSRQRSERCVE 261 : : : : : : : : : : : |
| DB | 205 NEFSIDVE---EGVSICYFFQAMIFSRKTQNONGSPGSTVCTE 243 : : : : : : : : : : : |

RESULT 15

| | |
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| ID | INGR HUMAN |
| ID | STANDARD; PRT; 489 AA. |
| AC | P15260; |
| DT | 01-APR-1990 (Rel. 14, Created) |
| DT | 01-APR-1990 (Rel. 14, last sequence update) |
| DT | 15-SEP-2003 (Rel. 42, last annotation update) |
| DE | Interferon-gamma receptor alpha chain precursor (CDw119). |
| OS | IFNGR1. |
| GN | Homo sapiens (Human). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |
| NCBI_Taxid | 9606; |
| RN | [1] |
| RX | SEQUENCE FROM N.A. |
| RX | MEDLINE=89003065; PubMed=2971451; |
| RA | Agnet M., Dembic Z., Merlin G.; |
| RT | "Molecular cloning and expression of the human interferon-gamma |
| RT | receptor."; |
| RL | Cell 55:273-280(1988). |
| RN | [2] |
| RA | SEQUENCE FROM N.A. |
| RP | Phillimore B.; |
| RL | Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases. |
| RN | [3] |

SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=2238257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McWen P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.
RX MEDLINE=93183911; PubMed=8443182;
RA Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Garotta G.;
RT "Alignment of disulfide bonds of the extracellular domain of the
interferon gamma receptor and investigation of their role in
RT biological activity."
RL Biochemistry 32:2423-2430(1993).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.
RX MEDLINE=95342235; PubMed=7617032;
RA Walter M.R., Windsor W.T., Nagabushan T.L., Lundell D.J., Lunn C.A.,
RA Zaucodny P.J., Narula S.K.;
RT "Crystal structure of a complex between interferon-gamma and its
soluble high-affinity receptor."
RL Nature 376:230-235(1995).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 IN COMPLEX WITH
ANTIBODY.
RX MEDLINE=98035727; PubMed=9367779;
RA Segabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,
RA Winkler F.K., Robinson J.A.;
RT "Neutralizing epitopes on the extracellular interferon gamma receptor
(IFNgamma) alpha-chain characterized by homolog scanning mutagenesis
and X-ray crystal structure of the A6 fab-IFNgamma1-108 complex."
RL J. Mol. Biol. 273:882-897(1997).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF COMPLEX WITH ING.
RX MEDLINE=20444407; PubMed=1098460;
RA Thiel D.J., Le Du M.-H., Walter R.L., D'Arcy A., Chene C.,
RA Fountoulakis M., Garotta G., Winkler F.K., Balick S.E.;
RT "Observation of an unexpected third receptor molecule in the crystal
structure of human interferon-gamma receptor complex."
RL Structure 8:927-936(2000).
CC -|- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE
INTERFERON-GAMMA DIMER.
CC -|- SUBUNIT: Monomer.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.
CC -|- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -|- SIMILARITY: Contains 2 fibronectin type III domains.
CC -|- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC -|- DATABASE: NAME=PROW; NOTE=CD guide CDw119 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw119.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J03143; AAA52731.1; --
CC EMBL: AL050337; CAB53062.1; --
CC EMBL: BC005333; AAH05333.1; --
CC PIR: A31555; A31555.
CC PDB: 1JRH; 25-MAR-98.
CC PDB: 1FG9; 29-NOV-00.
CC GlycoSuiteDB: P15260; --
CC Genew: HGNC:5439; IFNGR1.
CC MIM: 107470; --
CC MIM: 209950; --
CC GO: GO:0005887; C: integral to plasma membrane; TAS.
CC GO: GO:0003800; F: antiviral response protein activity; TAS.
CC GO: GO:0004906; F: interferon-gamma receptor activity; TAS.
CC GO: GO:0006955; P: immune response; TAS.
CC GO: GO:0009619; P: resistance to pathogenic bacteria; TAS.
CC GO: GO:0009615; P: response to viruses; TAS.
CC GO: GO:0007165; P: signal transduction; TAS.
CC InterPro: IPR000282; Cytok receptor 2.
KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Immunoglobulin domain; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 266 POTENTIAL.
FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).
FT DISULFID 77 85
FT DISULFID 122 167
FT DISULFID 195 200
FT DISULFID 214 235
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FT STRAND 98 106
FT TURN 107 108
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Query March 8.6%; Score 122.5; DB 1; Length 489;
Best Local Similarity 20.1%; Pred. No. 0.00091;
Matches 56; Conservative 49; Mismatches 103; Indels 71; Gaps 10;

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Db 50 YQIMPQVPVFTVEVKN-----YGVKNGSEWIDACINISHHYC 85
QY 119 DLTSETSDIQEPPYGRVRAASAGSYSEWSMTPTPWETKIDPPVNMNITQVNGSLVL 178
Db 86 NISDHVGDPSNLSLWVRKARVGOKESAIAKSEFAVCRDGKIGPKDIRKEEKQIMIDI 145
QY 179 HAPNLPYRQKXNVSIEDY-----YELLYRYFIIINNSLEKEQKVE-----GAH 223
Db 146 FHPSV-FVNGDEQEV---DYDPETTCYIRVYVYVVRMNGSEIQYKILTQKEDDCDEIQCQ 201
QY 224 RAVEIEALTPHSSYCVVAEIIYQPMLEDRRSORSEERCVEI 262
Db 202 LAIPVSSL--NSQYCVSAEGLHVWGVTTEKSKEVCITI 238

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Search completed: December 12, 2003, 12:26:06
Job time : 18.939 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 12:14:52 ; Search time 5.85763 Seconds
(without alignments)
1016.022 Million cell updates/sec

Title: US-10-047-264A-4_COPY_67_98
Perfect score: 188
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues
Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 188 | 100.0 | 263 | 11 | US-09-961-404-6 |
| 2 | 188 | 100.0 | 263 | 12 | US-10-047-264A-4 |
| 3 | 188 | 100.0 | 263 | 12 | US-10-293-832-28 |
| 4 | 188 | 100.0 | 263 | 12 | US-10-312-088-42 |
| 5 | 56.5 | 30.1 | 103 | 10 | US-09-764-864-1340 |
| 6 | 56.5 | 30.1 | 399 | 10 | US-09-764-864-891 |
| 7 | 52 | 27.7 | 20 | 9 | US-09-864-761-43449 |
| 8 | 52 | 27.7 | 63 | 11 | US-09-764-891-3345 |
| 9 | 51.5 | 27.4 | 107 | 12 | US-10-094-749-1942 |
| 10 | 51 | 27.1 | 63 | 10 | US-09-738-626-5085 |
| 11 | 51 | 27.1 | 183 | 9 | US-09-739-907-65 |
| 12 | 51 | 27.1 | 378 | 15 | US-10-188-012-33 |
| 13 | 51 | 27.1 | 378 | 15 | US-10-188-012-35 |
| 14 | 51 | 27.1 | 379 | 11 | US-09-813-153-138 |
| 15 | 51 | 27.1 | 995 | 11 | US-09-984-130-48 |

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| 16 | 51 | 27.1 | 995 | 12 | US-09-836-353A-48 | Sequence 48, Appl |
| 17 | 50 | 26.6 | 27 | 12 | US-10-354-047A-7 | Sequence 7, Appl |
| 18 | 50 | 26.6 | 88 | 12 | US-10-354-047A-18 | Sequence 18, Appl |
| 19 | 50 | 26.6 | 88 | 12 | US-10-354-047A-28 | Sequence 28, Appl |
| 20 | 50 | 26.6 | 89 | 15 | US-10-072-602B-23 | Sequence 23, Appl |
| 21 | 49 | 26.1 | 28 | 12 | US-10-354-047A-2 | Sequence 2, Appl |
| 22 | 49 | 26.1 | 28 | 15 | US-10-072-602B-24 | Sequence 24, Appl |
| 23 | 49 | 26.1 | 75 | 12 | US-10-403-340-4 | Sequence 4, Appl |
| 24 | 49 | 26.1 | 77 | 12 | US-10-403-340-5 | Sequence 5, Appl |
| 25 | 49 | 26.1 | 197 | 10 | US-09-764-864-1097 | Sequence 1097, Ap |
| 26 | 49 | 26.1 | 252 | 9 | US-09-764-903-50 | Sequence 50, Appl |
| 27 | 49 | 26.1 | 515 | 9 | US-09-895-072-6 | Sequence 6, Appl |
| 28 | 49 | 26.1 | 515 | 10 | US-09-986-552-6 | Sequence 6, Appl |
| 29 | 49 | 26.1 | 515 | 12 | US-10-023-834-18 | Sequence 18, Appl |
| 30 | 49 | 26.1 | 515 | 12 | US-10-024-197-18 | Sequence 18, Appl |
| 31 | 49 | 26.1 | 515 | 12 | US-10-306-686-6 | Sequence 6, Appl |
| 32 | 49 | 26.1 | 515 | 15 | US-10-023-888-18 | Sequence 18, Appl |
| 33 | 49 | 26.1 | 515 | 15 | US-10-023-889-18 | Sequence 18, Appl |
| 34 | 49 | 26.1 | 515 | 15 | US-10-023-890-18 | Sequence 18, Appl |
| 35 | 49 | 26.1 | 1143 | 10 | US-09-924-154-14 | Sequence 14, Appl |
| 36 | 48 | 25.5 | 16 | 12 | US-10-196-394-34 | Sequence 34, Appl |
| 37 | 48 | 25.5 | 88 | 12 | US-10-354-047A-34 | Sequence 34, Appl |
| 38 | 47.5 | 25.3 | 89 | 9 | US-09-864-761-34477 | Sequence 34477, A |
| 39 | 47.5 | 25.3 | 127 | 15 | US-10-155-886-49 | Sequence 49, Appl |
| 40 | 47.5 | 25.3 | 246 | 15 | US-10-155-886-16 | Sequence 16, Appl |
| 41 | 47.5 | 25.3 | 289 | 15 | US-10-286-264-110 | Sequence 110, App |
| 42 | 47.5 | 25.3 | 355 | 10 | US-09-925-300-1662 | Sequence 1662, Ap |
| 43 | 47.5 | 25.3 | 807 | 14 | US-10-138-221-7 | Sequence 7, Appl |
| 44 | 47 | 25.0 | 27 | 12 | US-10-354-047A-10 | Sequence 10, Appl |
| 45 | 47 | 25.0 | 27 | 12 | US-10-354-047A-16 | Sequence 16, Appl |

ALIGNMENTS

RESULT 1
US-09-961-404-6
; Sequence 6, Application US/09961404
; Publication No. US20030022827A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: SABAT, ROBERT
; APPLICANT: ASADULLAH, KHUSRU
; APPLICANT: TOSCHI, LUISELLA
; TITLE OF INVENTION: THREE NEW MEMBERS OF THE CYTOKINE RECEPTOR
; FILE REFERENCE: SCH-1788
; CURRENT APPLICATION NUMBER: US/09/961,404
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-404-6

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|--|--------------|------------------------------------|---------------|-------------|
| Query Match | 100.0% | Score 188; | DB 11; | Length 263; |
| Best Local Similarity | 100.0% | Pred. No. 5.5e-16; | Mismatches 0; | Indels 0; |
| Matches 32; | Conservative | 0; | Length 263; | |
| QY | 1 | MFSCSMKSHQKPSGQWQHISCNFPFCRTLAK 32 | | |
| DB | 67 | MFSCSMKSHQKPSGQWQHISCNFPFCRTLAK 98 | | |
| RESULT 2 | | | | |
| US-10-047-264A-4 | | | | |
| ; Sequence 4, Application US/10047264A | | | | |
| ; Publication No. US20030170839A1 | | | | |
| ; GENERAL INFORMATION: | | | | |
| ; APPLICANT: Fousseur, Lynette | | | | |
| ; APPLICANT: Liu, Wei | | | | |

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; APPLICANT: Deng, Bijia
; TITLE OF INVENTION: TYPE 2 CYTOKINE RECEPTOR AND NUCLEIC ACIDS ENCODING
; FILE REFERENCE: 22058-532
; CURRENT APPLICATION NUMBER: US/10/047,264A
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/261442
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/267021
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/270835
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 263
; TYPE: PRT
; ORGANISM: human
US-10-047-264A-4

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Best Local Similarity 100.0%; Pred. No. 5.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MFSCSMKSSHQKPGSGCQWQHISCNFPFGCRTLAK 32
Db      67 MFSCSMKSSHQKPGSGCQWQHISCNFPFGCRTLAK 98

RESULT 3
US-10-293-832-28
; Sequence 28, Application US/10293832
; Publication No. US20030180752A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Wei
; APPLICANT: Fouser, Lynette
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: TYPE 2 CYTOKINE RECEPTOR AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 22058-546
; CURRENT APPLICATION NUMBER: US/10/293,832
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/332,366
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-832-28

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Best Local Similarity 100.0%; Pred. No. 5.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      67 MFSCSMKSSHQKPGSGCQWQHISCNFPFGCRTLAK 98

RESULT 4
US-10-312-088-42
; Sequence 42, Application US/10312088
; Publication No. US20030219862A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Cogswell, John P.
; APPLICANT: Kabnic, Karen S.
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Martensen, Shelby A.
; APPLICANT: Murdock, Paul R.
; APPLICANT: Smith, Randall F.
; APPLICANT: Strum, Jay C.
```

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; APPLICANT: Xiang, Zhaoying
; APPLICANT: Xie, Qing
; APPLICANT: Rizni, Safia K.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50029
; CURRENT APPLICATION NUMBER: US/10/312,088
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/19929
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,161
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/213,156
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-088-42

Query Match      100.0%; Score 188; DB 12; Length 263;
Best Local Similarity 100.0%; Pred. No. 5.5e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MFSCSMKSSHQKPGSGCQWQHISCNFPFGCRTLAK 32
Db      67 MFSCSMKSSHQKPGSGCQWQHISCNFPFGCRTLAK 98

RESULT 5
US-09-764-864-1340
; Sequence 1340, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1340
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (95)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1340

Query Match      30.1%; Score 56.5; DB 10; Length 103;
Best Local Similarity 39.3%; Pred. No. 7.9;
Matches 11; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

Qy      8 SSHQKPSG---CQWQHISCNFPFGCRTLAK 32
Db      11 SSHEETPGSHPLYGHGECRWPGCETLCE 38

RESULT 6
US-09-764-864-891
; Sequence 891, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
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; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 891
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-891

Query Match          30.1%; Score 56.5; DB 10; Length 399;
Best Local Similarity 39.3%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

QY 8 SSGHPSG--CWOHISCNPFPGCRTLAK 32
Db 11 SSHEETPGSHPLYGHGCKWPGCETLCE 38

RESULT 7
US-09-864-761-43449
; Sequence 43449, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43449
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; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006249.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.59
; OTHER INFORMATION: EST_HUMAN HIT: AAL34017.1, EVALUE 2.20e-02
US-09-864-761-43449

Query Match          27.7%; Score 52; DB 9; Length 20;
Best Local Similarity 52.4%; Pred. No. 6.5;
Matches 11; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 10 HQKPSGCWQHISCNPFPGCRTL 30
Db 1 HQKLSRRWCHASCT--ACRTM 19

RESULT 8
US-09-764-891-3345
; Sequence 3345, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3345
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (19)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (45)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3345

Query Match          27.7%; Score 52; DB 11; Length 63;
Best Local Similarity 42.1%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 5 SMKSSHQKPSGCWQHISCN 23
Db 21 SMLRSYNTGSCWSHCKCN 39

RESULT 9
US-10-094-749-1942
; Sequence 1942, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUOI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
```

APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1942
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-1942

Query Match 27.4%; Score 51.5; DB 12; Length 107;
Best Local Similarity 43.5%; Pred. No. 35;
Matches 10; Conservative 1; Mismatches 7; Indels 5; Gaps 1;

QY 9 SHQKPSGCWQHISCNPFPCRTLA 31
DB 70 SHTHISCN-----NFFSCHVLS 87

RESULT 10
US-09-738-626-5085
Sequence 5085, Application US/09738626
Publication No. US20020197603A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 5085
LENGTH: 63
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5085

Query Match 27.1%; Score 51; DB 10; Length 63;
Best Local Similarity 33.3%; Pred. No. 25;
Matches 9; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 2 FSCSMKSSHQKPSGCWQHISCNPFPGCR 28
DB 33 YAAAWESAHLKATSOEVFSCEFLGCR 59

RESULT 11
US-09-739-907-65
Sequence 65, Application US/09739907
Patent No. US20010012889A1
GENERAL INFORMATION:
APPLICANT: ROSEN ET AL.
TITLE OF INVENTION: 36 Human Secreted Proteins
FILE REFERENCE: P2022P1
CURRENT APPLICATION NUMBER: US/09/739,907
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/348,457
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: 60/070,567
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,692
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,704
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 65
LENGTH: 183
TYPE: PRT
ORGANISM: Homo sapiens
US-09-739-907-65

Query Match 27.1%; Score 51; DB 9; Length 183;
Best Local Similarity 40.0%; Pred. No. 66;
Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 9 SHQKPSGCWQHISCNPFPGCR 28
DB 46 SHNSNSMCWKGKDCQPYSGCK 65

RESULT 12
US-10-188-012-33
Sequence 33, Application US/10188012
Publication No. US20030124114A1
GENERAL INFORMATION:
APPLICANT: McIntire, Jennifer Jones
APPLICANT: Umetsu, Dale T.
APPLICANT: Dekruyff, Rosemarie
APPLICANT: Kuchroo, Vijay
APPLICANT: Freeman, Gordon J.
TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
FILE REFERENCE: STAN-235
CURRENT APPLICATION NUMBER: US/10/188,012
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/302,344
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 378
TYPE: PRT
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(378)
OTHER INFORMATION: TIM-4, allele 1
US-10-188-012-33

Query Match 27.1%; Score 51; DB 15; Length 378;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;

Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 9 SHQKPSGCWQHISCNFPGCR 28
Db 46 SHNSNSMCWKGKDCPYSGCK 65

RESULT 13

US-10-188-012-35
; Sequence 35, Application US/10188012
; Publication No. US20030124114A1
; GENERAL INFORMATION:
; APPLICANT: McIntire, Jennifer Jones
; APPLICANT: Umetsu, Dale T.
; APPLICANT: Dekruyff, Rosemarie
; APPLICANT: Kuchroo, Vijay
; APPLICANT: Freeman, Gordon J.
; TITLE OF INVENTION: T Cell Regulatory Genes and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: STAN-235
; CURRENT APPLICATION NUMBER: US/10/188,012
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/302,344
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 378
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(378)
; OTHER INFORMATION: TIM-4, allele 2
US-10-188-012-35

Query Match 27.1%; Score 51; DB 15; Length 378;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 9 SHQKPSGCWQHISCNFPGCR 28
Db 46 SHNSNSMCWKGKDCPYSGCK 65

RESULT 14

US-09-813-153-138
; Sequence 138, Application US/09813153
; Publication No. US20030045459A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023
; CURRENT APPLICATION NUMBER: US/09/813,153
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: US/09/363,044
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,170
; PRIOR FILING DATE: 1998-01-30

; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 138
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (379)
; OTHER INFORMATION: Xaa equals stop translation
US-09-813-153-138

Query Match 27.1%; Score 51; DB 11; Length 379;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

Qy 9 SHQKPSGCWQHISCNFPGCR 28
Db 46 SHNSNSMCWKGKDCPYSGCK 65

RESULT 15

US-09-984-130-48
; Sequence 48, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 995
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-48

Query Match 27.1%; Score 51; DB 11; Length 995;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 12 KPSGCWQHISCNFPGCR 29
Db 3 KPTPNSERSVSRPFGCR 20

Search completed: December 12, 2003, 12:24:05
Job time : 5.85763 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 12:15:52 ; Search time 8.13559 Seconds
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624.325 Million cell updates/sec

Title: US-10-047-264A-4_COPY_67_98

Perfect score: 188

Sequence: 1 MFSCSMKSHQPSGCMQWHSFCNFPQCRTLAK 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|--------------------|
| 1 | 188 | 100.0 | 262 | 22 AAU09186 | Human PRO19598 pol |
| 2 | 188 | 100.0 | 263 | 23 ABU10499 | Cytokine receptor |
| 3 | 188 | 100.0 | 263 | 23 AA017382 | Human cytokine rec |
| 4 | 188 | 100.0 | 263 | 23 AA017321 | Human cytokine rec |
| 5 | 153 | 81.4 | 263 | 23 AAU03034 | Human IL-TIF/IL-22 |
| 6 | 56.5 | 30.1 | 103 | 22 AAU16387 | Human novel polype |
| 7 | 56.5 | 30.1 | 103 | 24 ABUS5456 | Human novel polype |
| 8 | 56.5 | 30.1 | 399 | 22 AAU15938 | Human novel secret |
| 9 | 56.5 | 30.1 | 399 | 24 ABUS55007 | Human novel polype |

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| 10 | 56.5 | 30.1 | 668 | 23 | AAE25288 | Human nucleic acid |
| 11 | 55 | 29.3 | 761 | 20 | AAW70899 | Protein encoded by |
| 12 | 55 | 29.3 | 761 | 21 | AAV44704 | Human tumour suppr |
| 13 | 53 | 28.2 | 105 | 22 | AU42091 | Propionibacterium |
| 14 | 52 | 27.7 | 20 | 22 | ABG53249 | Human liver peptid |
| 15 | 52 | 27.7 | 20 | 22 | ABG38426 | Peptide #5932 enco |
| 16 | 52 | 27.7 | 20 | 22 | AAW59036 | Human brain expres |
| 17 | 52 | 27.7 | 20 | 22 | AAW71567 | Human bone marrow |
| 18 | 52 | 27.7 | 20 | 22 | AAW31865 | Peptide #5902 enco |
| 19 | 52 | 27.7 | 20 | 23 | ABG41379 | Human peptide enco |
| 20 | 52 | 27.7 | 63 | 22 | AAW94687 | Human reproductive |
| 21 | 52 | 27.7 | 308 | 22 | AAU51635 | Propionibacterium |
| 22 | 52 | 27.7 | 316 | 16 | AAW94345 | Hepatitis GB virus |
| 23 | 51.5 | 27.4 | 1008 | 22 | ABG11527 | Human apolipoprote |
| 24 | 51.5 | 27.4 | 1013 | 22 | ABG08112 | Novel human diagno |
| 25 | 51 | 27.1 | 63 | 22 | AAW91331 | C Glutamicum prote |
| 26 | 51 | 27.1 | 124 | 22 | ABG11089 | Human secreted pro |
| 27 | 51 | 27.1 | 144 | 22 | AAU53344 | Propionibacterium |
| 28 | 51 | 27.1 | 183 | 20 | AAW38395 | Human secreted pro |
| 29 | 51 | 27.1 | 378 | 22 | AAW39027 | Human polypeptide |
| 30 | 51 | 27.1 | 378 | 24 | ABP70446 | Amino acid sequenc |
| 31 | 51 | 27.1 | 378 | 24 | ABP70447 | Human secreted pro |
| 32 | 51 | 27.1 | 379 | 20 | AAW25768 | Mycobacterium spec |
| 33 | 50.5 | 26.9 | 148 | 20 | AAW04799 | Novel human diagno |
| 34 | 50.5 | 26.9 | 154 | 22 | ABG11413 | Novel human diagno |
| 35 | 50.5 | 26.9 | 234 | 20 | AAW04813 | Mycobacterium spec |
| 36 | 50 | 26.6 | 27 | 22 | AAU03908 | P-superfamily cono |
| 37 | 50 | 26.6 | 88 | 22 | AAU03915 | P-superfamily cono |
| 38 | 50 | 26.6 | 88 | 22 | AAU03920 | P-superfamily cono |
| 39 | 50 | 26.6 | 89 | 23 | ABG99374 | Conus sp conotoxin |
| 40 | 50 | 26.6 | 358 | 22 | AAU60034 | Propionibacterium |
| 41 | 50 | 26.6 | 443 | 22 | ABG03615 | Novel human diagno |
| 42 | 49.5 | 26.3 | 190 | 21 | AAW18278 | Arabidopsis thalia |
| 43 | 49.5 | 26.3 | 192 | 21 | AAW49802 | Arabidopsis thalia |
| 44 | 49.5 | 26.3 | 307 | 21 | AAW18277 | Arabidopsis thalia |
| 45 | 49.5 | 26.3 | 309 | 21 | AAW49801 | Arabidopsis thalia |

ALIGNMENTS

RESULT 1

AAU09186

ID AAU09186 standard; Protein; 262 AA.

XX AAU09186;

AC AAU09186;

XX 16-JAN-2002 (first entry)

DT Human PRO19598 polypeptide.

DE Human; PRO19598; clone DNA145887; immune-related disorder;

XX Human; PRO19598; clone DNA145887; immune-related disorder;

KW inflammatory disorder; infectious disorder; immunodeficiency disorder;

KW autoimmune disorder; renal disease; demyelinating disease; skin disease;

KW neoplasia; transplantation associated disease; immunosuppressive;

KW anti-inflammatory; antiasthmatic; antidiabetic.

XX Homo sapiens.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..20

FT /label= Signal_peptide

FT Modified-site 17..22

FT /note= "N-myristoylation site"

FT Modified-site 20..25

FT /note= "N-myristoylation site"

FT Protein 21..262

FT /label= Mature_PRO19598_polypeptide

FT Modified-site 55..58

FT /note= "N-glycosylation site"

FT Modified-site 165..168

FT /note= "N-glycosylation site"

FT Modified-site 170..173

FT Modified-site /note= "N-glycosylation site"
 FT 191..194
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 FT 208..211
 FT Modified-site /note= "N-glycosylation site"
 FT 220..225
 FT Modified-site /note= "N-myristoylation site"
 FT 220..225
 XX WO200166740-A2.
 XX 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001WO-US066666.
 XX
 PR 03-MAR-2000; 2000US-187202P.
 PR 21-MAR-2000; 2000US-191015P.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 05-JUN-2000; 2000US-209832P.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 01-DEC-2000; 2000WO-US32678.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Eaton DL, Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 XX WPI; 2001-625876/72.
 DR N-PSDB; AAS15368.
 XX

Nucleic acids encoding PRO polypeptides, useful for detecting and treating immune related diseases and disorders in mammals including autoimmune diseases, inflammatory diseases and asthma -
 Claim 10; Fig 18; 122pp; English.

The present invention relates to the isolation of 9 novel human PRO polypeptides and the cDNA sequences (AAS15360-AAS15368) encoding them. The novel PRO polypeptides include PRO1356, PRO1268, PRO1884, PRO3444, PRO3151, PRO4322, PRO9964, PRO10008 and PRO19598. The cDNA sequences encoding these PRO polypeptides have been designated as clones DNA64886-1601, DNA64903-1553, DNA84318-2520, DNA87997, DNA89273, DNA92223-2567, DNA96973, DNA101921 and DNA145887 respectively. Compositions (e.g. vaccines) containing PRO polypeptides and methods of using these compositions are useful in the treatment and diagnosis of immune-related disorders. Such disorders include immune-mediated inflammatory disorders (e.g. osteoarthritis), non-immune-mediated inflammatory disorders (e.g. diabetes mellitus), infectious disorders (e.g. granulomatous hepatitis), immunodeficiency disorders (e.g. AIDS), autoimmune disorders (e.g. rheumatoid arthritis), immune-related renal diseases (e.g. cirrhosis), demyelinating diseases of the peripheral or central nervous system (e.g. Guillain-Barre syndrome), immune-mediated skin diseases (e.g. contact dermatitis), neoplasias and transplantation associated diseases. The polynucleotide sequences of the invention may be used in gene therapy. AAU09178-AAU09186 represent the novel human PRO polypeptides of the invention.

XX Sequence 262 AA;

Query Match 100.0%; Score 188; DB 22; Length 262;
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFSCSMKSSHQKPSGCWQHISCNFPFGCRTLAK 32
 |||||
 DB 66 MFSCSMKSSHQKPSGCWQHISCNFPFGCRTLAK 97

RESULT 2
 ABJ10499
 ID ABJ10499 standard; Protein; 263 AA.
 XX
 AC ABJ10499;
 XX

DT 21-NOV-2002 (first entry)
 XX
 DE Cytokine receptor family 2 (CRF2) related protein SEQ ID No 4.
 XX
 KW Immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; interleukin-antagonist-20; interleukin-antagonist-22;
 KW gene therapy; interferon-antagonist-alpha; interferon-antagonist-beta;
 KW interferon-antagonist-gamma; cytokine receptor family 2; CRF2-12;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW inflammation.
 XX
 OS Unidentified.
 XX
 XX WO200266647-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 14-JAN-2002; 2002WO-US00986.
 XX
 PR 12-JAN-2001; 2001US-261442P.
 PR 06-FEB-2001; 2001US-267021P.
 PR 23-FEB-2001; 2001US-270835P.
 XX
 XX (GEMY) GENETICS INST LLC.
 PA
 XX Fouser L, Liu W, Deng B;
 PI
 XX WPI; 2002-674946/72.
 DR N-PSDB; ABO8217.
 XX
 PT New isolated CRF2-12 nucleic acid encoding a polypeptide, useful for
 PT diagnosing and treating disorders with abnormal CRF2-12 activity such
 PT as autoimmune diseases like rheumatoid arthritis, multiple sclerosis
 PT and inflammation -
 PT
 XX Claim 2; Page 7; 91pp; English.
 PS
 CC The invention relates to an isolated type 2 cytokine receptor family
 CC (CRF2-12) nucleic acid molecule encoding a polypeptide with amino acids
 CC 21-66 of a 231 residue amino acid sequence, given in the specification,
 CC or its complement. The compositions and methods of the present invention
 CC are useful for diagnosing, screening and treating disorders associated
 CC with abnormal CRF2-12 activity such as autoimmune diseases like
 CC rheumatoid arthritis, multiple sclerosis and inflammation. This sequence
 CC represents a cytokine receptor family 2 (CRF2-12) protein relating to the
 CC invention.
 XX
 SQ Sequence 263 AA;
 Query Match 100.0%; Score 188; DB 23; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1.6e-17;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFSCSMKSSHQKPSGCWQHISCNFPFGCRTLAK 32
 |||||
 DB 67 MFSCSMKSSHQKPSGCWQHISCNFPFGCRTLAK 98

RESULT 3
 AAO17382
 ID AAO17382 standard; Protein; 263 AA.

XX AAO17382;
 AC
 XX
 DT 08-AUG-2002 (first entry)
 XX
 DE Human cytokine receptor variant 3.

XX Human; cytokine receptor; immune disease; psoriasis; cancer; infection;
 KW rheumatoid arthritis; multiple sclerosis; Crohn's disease;
 KW ulcerative colitis; transplant rejection; abortion; antipsoriatic;
 KW immunosuppressive; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiulcer; cytostatic; dermatological;

KW chromosome 6q24.1-25.2; receptor.
 XX Homo sapiens.
 XX EP1191035-A2.
 XX 27-MAR-2002.
 XX 24-AUG-2001; 2001EP-0250307.
 XX 25-SEP-2000; 2000DE-1048626.
 XX 17-NOV-2000; 2000DE-1058907.
 XX 19-DEC-2000; 2000DE-1064906.
 XX (SCHD) SCHERING AG.
 XX Weiss B, Sabat R, Assadullah K, Toshi L;
 XX WPI; 2002-332210/37.
 DR N-PSDB; AAL46001.
 XX New nucleic acid encoding soluble cytokine receptor, useful for
 PT diagnosis and treatment of e.g. immune disease, also related protein
 PT and antibodies
 XX Claim 6; Page 15; 21pp; German.
 XX The present invention provides the protein and coding sequences of 3
 CC variants of a human cytokine receptor. The sequences can be used in the
 CC diagnosis, prevention and treatment of immune diseases, including
 CC psoriasis, cancer, chronic/life-threatening infections, rheumatoid
 CC arthritis, multiple sclerosis, Crohn's disease, ulcerative colitis and
 CC transplant rejection and in reproductive medicine, e.g. for diagnosing
 CC abnormal immune reactions which cause abortions. The present sequence is
 CC variant 3 of the invention.
 XX SQ Sequence 263 AA;
 Query Match 100.0%; Score 188; DB 23; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1.6e-17;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFSCSMKSSHQKPGSGCQWHISCNFPFGCRTLAK 32
 Db 67 MFSCSMKSSHQKPGSGCQWHISCNFPFGCRTLAK 98
 RESULT 4
 AAE17321
 ID AAE17321 standard; Protein; 263 AA.
 XX AAE17321;
 AC AAE17321;
 XX 18-APR-2002 (first entry)
 DT Human cytokine receptor protein, sbg456548Cytora #3.
 XX Human; therapy; wound healing disorder; vaccine; cancer; infection;
 KW autoimmune disorder; haematopoietic disorder; inflammation; arthritis;
 KW Parkinson's disease; Huntington's chorea; schizophrenia; antiarrhythmic;
 KW multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma;
 KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;
 KW depression; cardiovascular disease; myocardial infarction; renal failure;
 KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;
 KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;
 KW hyperlipidemia; renal disease; hypoglycaemia; gastrointestinal disease;
 KW neotrophic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
 KW haemostatic; vulnery; anticonvulsant; antirheumatic; neuroprotective;
 KW nephrotropic; hypotensive; vasotropic; cytostatic; cerebroprotective;
 KW allergy; cytokine receptor.
 OS Homo sapiens.
 XX

PN WO200198342-A1.
 XX 27-DEC-2001.
 XX 22-JUN-2001; 2001WO-US19929.
 XX 22-JUN-2000; 2000US-213156P.
 PR 22-JUN-2000; 2000US-213161P.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX (GLAX) GLAXO GROUP LTD.
 PI Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;
 PI Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;
 XX WPI; 2002-139783/18.
 DR N-PSDB; AAD27816.
 XX Novel secreted and membrane-associated polypeptides and polynucleotides
 PT useful for preventing, ameliorating or correcting dysfunction or
 PT disease including diabetes, cancer, hypertension and growth
 PT abnormalities
 XX Claim 1; Page 133-134; 138pp; English.
 XX The invention relates to secreted and membrane-associated polypeptides
 CC and polynucleotides. The sequences of the invention are useful in
 CC diagnostic assays for detecting diseases associated with inappropriate
 CC activity or levels of these polynucleotides, and in identifying their
 CC agonists and antagonists that are potentially useful in therapy. The
 CC sequences of the invention are useful as vaccines for inducing
 CC immunological response. The sequences of the invention are useful for
 CC treating cancers, infections, autoimmune disorders, haematopoietic
 CC disorders, wound healing disorders, cholesterol ester storage disease,
 CC inflammation, congenital muscular dystrophy, junctional epidermolysis
 CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,
 CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,
 CC septicemia, psoriasis, inflammatory bowel disease, acute respiratory disease,
 CC graft versus host disease, ischaemia, stroke, bone diseases, atherosclerosis,
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, myotonic dystrophy,
 CC brain disorders including parasupranuclear palsy, myotonic dystrophy,
 CC depression, anxiety disorders and sleep disorders, cardiovascular
 CC diseases including congestive heart failure and myocardial infarction,
 CC respiratory diseases including chronic obstructive pulmonary disease,
 CC acute bronchitis and adult respiratory distress syndrome, liver disorders
 CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral
 CC and non-viral hepatitis, type II diabetes mellitus, renal disease
 CC including acute and chronic renal failure, glomerulonephritis, Fanconi's
 CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia
 CC and tendinitis, gastrointestinal diseases including intestinal
 CC obstruction and tropical sprue, spleen disorders including hypersplenism,
 CC Hodgkin's disease and malignant lymphoma, testicular cancer, male
 CC reproductive diseases including low testosterone and male infertility.
 CC The present sequence is human cytokine receptor.
 XX SQ Sequence 263 AA;
 Query Match 100.0%; Score 188; DB 23; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1.6e-17;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MFSCSMKSSHQKPGSGCQWHISCNFPFGCRTLAK 32
 Db 67 MFSCSMKSSHQKPGSGCQWHISCNFPFGCRTLAK 98
 RESULT 5
 AAU80324
 ID AAU80324 standard; Protein; 263 AA.
 XX AAU80324;
 AC AAU80324;

XX 15-JUL-2002 (first entry)
 XX Human IL-TIF/IL-22 binding protein #2.
 DE Human; soluble protein; interleukin-TIF/IL-22; IL-TIF/IL-22; IL-22BP;
 XX IL-TIF/IL-22 antagonist.
 KW Homo sapiens.
 OS WO200224912-A2.
 FN 28-MAR-2002.
 PD 21-SEP-2001; 2001WO-US29576.
 PF 22-SEP-2000; 2000US-234583P.
 XX 03-NOV-2000; 2000US-245495P.
 PR 31-JUL-2001; 2001US-0919162.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Renaud J, Dumoutier L;
 PI WPI; 2002-383190/41.
 DR N-PSDB; ABK50080.
 XX Polynucleotide and polypeptide of soluble protein which binds to
 PT interleukin-TIF/IL-22 useful for inhibiting effect of IL-TIF/IL-22 on a
 PT cell -
 XX Claim 14; Page 41-42; 42pp; English.
 PS The present invention relates to a new polynucleotide that encodes a
 CC soluble protein which binds to interleukin (IL)-TIF/IL-22 (also referred
 CC to as IL-22BP), where the complementary sequence of the invention
 CC hybridises under stringent conditions to a nucleotide sequence of 2271
 CC or 2366 base pairs, as given in the specification. The molecules of the
 CC invention are useful for inhibiting (antagonising) effect of IL-TIF/IL-22
 CC on a cell, for determining whether IL-TIF/IL-22 is present in a sample,
 CC for inhibiting binding of IL-TIF/IL-22 to a binding partner, preferably
 CC in vitro, and for obtaining an antibody molecule specific for the soluble
 CC binding protein of the invention, from a population or panel of antibody
 CC molecules of diverse binding specificity. The soluble protein is further
 CC useful in manufacture of a medicament for treating an IL-22 mediated
 CC disease and for assaying an agent, preferably an antibody or a peptide
 CC fragment of IL-TIF/IL-22 or the soluble protein, that modulates binding
 CC of the soluble protein to IL-TIF/IL-22, where the agent identified is
 CC used in the manufacture of medicament for treating IL-TIF/IL-22 mediated
 CC disorder. The antibody is useful for determining presence of the soluble
 CC protein, where the antibody is detectably labelled. The present amino
 CC acid sequence represents the human IL-TIF/IL-22 binding protein #2 of
 CC the invention.
 XX SQ Sequence 263 AA;
 Query Match 81.4%; Score 153; DB 23; Length 263;
 Best Local Similarity 84.4%; Pred. No. 8.8e-13;
 Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MFSCSMKSSHQPSGCGWQHICNFPFGCRTLAK 32
 |||||
 Db 67 MFSCSMKSSHQPSGCGWQHICNFPFGCRTLAK 98
 RESULT 6
 AAU16387
 ID AAU16387 standard; Protein, 103 AA.
 XX
 AC AAU16387;
 XX
 DT 07-NOV-2001 (first entry)
 XX

DE Human novel secreted protein, Seq ID 1340.
 XX Human; immunosuppressive; antiarthritic; antirheumatic;
 KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
 KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
 KW vulnary; secreted protein; rheumatoid arthritis;
 KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
 KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
 KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
 KW corneal infection; wound healing; epithelial cell proliferation;
 KW skin ageing; food additive; preservative; antiproliferative.
 XX Homo sapiens.
 OS WO200155322-A2.
 FN 02-AUG-2001.
 PD 17-JAN-2001; 2001WO-US01341.
 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 14-JUL-2000; 2000US-0217496.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.

292 SSHEETPGSHPLYGHGECKWPCGCTLCE 319

Dd ||||| :||| ||| |
RESULT 11
AAW70899
ID AAW70899 standard; Protein; 761 AA.
XX AC AAW70899;
AC XX
DT DT 09-MAR-1999 (first entry)
XX DE
DE DE Protein encoded by tumour suppressor gene IB3089A.
XX KW Tumour suppressor gene; IB3089A; DBCCR1; q32-33; hypermethylation;
KW Deleted in Bladder Cancer Chromosome Region candidate 1; cancer;
KW bladder cancer; ovarian cancer; skin cancer; squamous carcinoma;
KW renal cell carcinoma; squamous cell oesophageal carcinoma;
KW prenatal testing; heterozygosity loss.
XX OS Homo sapiens.
OS XX
PN PN WO9854318-A1.
PN XX
PD PD 03-DEC-1998.
PD XX
PF PF 26-MAY-1998; 98WO-CB01515.
PF XX
PR PR 28-MAY-1997; 97GB-0010995.
PR XX
PA PA (CURI-) CURIE RES INST MARIE.
PI PI Habuchi T, Knowles M,
XX DR WFI; 1999-070216/06.
DR N-PSDB; AAV83819.
XX PT New human gene, DBCCR1, associated with bladder and other cancers -
PT used for diagnosis, treatment and prevention of cancer
XX FS Claim 2; Fig 6; 106pp; English.

CC The present sequence is encoded by tumour suppressor gene IB3089A,
CC also known as DBCCR1 (Deleted in Bladder Cancer Chromosome Region
CC candidate 1). The gene is located at q32-33. Although the gene is
CC expressed in multiple human tissues, lack of expression of the gene was
CC found in several bladder cancer cells. The DBCCR1 gene is involved in
CC the development of sporadic cancer, probably by the deletion of one
CC allele of the gene and/or hypermethylation of the remaining allele,
CC leading to reduced expression of the gene. DBCCR1 nucleic acid sequences
CC are used for treatment or prevention of cancer, particularly bladder,
CC ovarian or skin cancer, squamous carcinoma, renal cell carcinoma or
CC squamous cell oesophageal carcinoma. The DBCCR1 protein can be used
CC directly in the same way, or used to raise antibodies and to screen
CC for modulators. The products can be used for diagnosis or prognosis of
CC cancer, or to indicate predisposition to cancer (including prenatal
CC testing), particularly where this is associated with loss of
CC heterozygosity at q32-33. Antibodies may also be used for affinity
CC purification, therapeutically as modulator and to detect the protein in
CC cells etc.
XX SQ Sequence 761 AA;

Query Match 29.3%; Score 55; DB 20; Length 761;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps

OY 5 SMKSSHOKPSCGWQHSICNF 24
Dd 19 SVQPQHGFAGTDQHVSKEF 38

RESULT 12

KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.

XX Homo sapiens.

OS WO200157273-A2.

PN WO200157273-A2.

PD 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00664.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-488998/53.

DR Human genome-derived single exon nucleic acid probes useful for

PT analysing gene expression in human adult liver -

XX Claim 27; SEQ ID No 31897; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SEN) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult
 CC liver (I) may be used for predicting, measuring and displaying gene
 CC expression in samples derived from human adult liver. The genes
 CC identified may be involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
 CC is associated with coronary heart disease. ABG47348-ABG59930 represent
 CC human liver single exon encoded peptides of the invention.
 CC Note: The sequence information for this patent does not appear in the
 CC printed specification but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 20 AA;

Query Match 27.7%; Score 52; DB 22; Length 20;

Best Local Similarity 52.4%; Pred. No. 3.4;

Matches 11; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 10 HOKPSGCWOHISCNPPGCRRL 30

Db 1 HOKLSRRWCHASCT--ACRTM 19

RESULT 15

ABB38426

ID ABB38426 standard; Peptide; 20 AA.

XX ABB38426;

XX 04-FEB-2002 (first entry)

DE Peptide #5932 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US00669.

XX

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-483447/52.

DR Human genome-derived single exon nucleic acid probes useful for

PT analysing gene expression in human foetal liver -

XX Claim 27; SEQ ID NO 31061; 639pp + sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC foetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 20 AA;

Query Match 27.7%; Score 52; DB 22; Length 20;

Best Local Similarity 52.4%; Pred. No. 3.4;

Matches 11; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 10 HOKPSGCWOHISCNPPGCRRL 30

Db 1 HOKLSRRWCHASCT--ACRTM 19

Search completed: December 12, 2003, 12:25:34

Job time : 9.13559 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 12:22:23 ; Search time 6.61695 Seconds
(without alignments)
1247.959 Million cell updates/sec

Title: US-10-047-264A-4_COPY_67_98

Perfect score: 188

Sequence: 1 MFSCSMKSHQKPSGQWQHISCNFPFGCRTLAK 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 188 | 100.0 | 263 | 4 Q969J5 | Q969J5 homo sapien |
| 2 | 61 | 32.4 | 367 | 16 Q8CX51 | Q8CX51 leptospira |
| 3 | 59.5 | 31.6 | 54 | 4 Q14230 | Q14230 homo sapien |
| 4 | 58.5 | 31.1 | 515 | 12 Q8B121 | Q8B121 latino viru |
| 5 | 58.5 | 31.1 | 515 | 12 Q8B116 | Q8B116 latino viru |
| 6 | 57.5 | 30.6 | 206 | 16 Q9CK78 | Q9CK78 pasteurella |
| 7 | 56.5 | 30.1 | 383 | 4 Q96AP5 | Q96AP5 homo sapien |
| 8 | 56.5 | 30.1 | 667 | 4 Q8IWE5 | Q8IWE5 homo sapien |
| 9 | 56.5 | 30.1 | 680 | 4 Q8IVH2 | Q8IVH2 homo sapien |
| 10 | 56.5 | 30.1 | 742 | 5 Q8I8V3 | Q8I8V3 giardia lam |
| 11 | 55 | 29.3 | 228 | 4 Q8WX56 | Q8WX56 homo sapien |
| 12 | 55 | 29.3 | 320 | 4 Q8WU22 | Q8WU22 homo sapien |
| 13 | 55 | 29.3 | 760 | 11 Q925T8 | Q925T8 rattus norv |
| 14 | 55 | 29.3 | 761 | 4 Q6O477 | Q6O477 homo sapien |
| 15 | 54.5 | 29.0 | 367 | 13 Q90XF6 | Q90XF6 brachydanio |
| 16 | 54 | 28.7 | 162 | 2 Q9L768 | Q9L768 desulfovibr |

| | | | | | |
|----|------|------|------|-----------|--------------------|
| 17 | 53.5 | 28.5 | 672 | 11 Q8CG10 | Q8CG10 mus musculu |
| 18 | 53.5 | 28.5 | 685 | 11 Q8CIS1 | Q8CIS1 mus musculu |
| 19 | 53.5 | 28.5 | 795 | 11 Q9DBY0 | Q9DBY0 mus musculu |
| 20 | 53 | 28.2 | 132 | 4 Q00504 | Q00504 homo sapien |
| 21 | 53 | 28.2 | 247 | 4 Q8NZX0 | Q8NZX0 homo sapien |
| 22 | 53 | 28.2 | 314 | 2 Q68475 | Q68475 xanthomonas |
| 23 | 53 | 28.2 | 445 | 4 Q8I2D0 | Q8I2D0 homo sapien |
| 24 | 53 | 28.2 | 528 | 11 Q8KOR2 | Q8KOR2 mus musculu |
| 25 | 51 | 27.1 | 63 | 16 Q8NQJ8 | Q8NQJ8 corynebacte |
| 26 | 51 | 27.1 | 118 | 11 Q89028 | Q89028 mus musculu |
| 27 | 51 | 27.1 | 167 | 2 Q59338 | Q59338 desulfovibr |
| 28 | 51 | 27.1 | 174 | 11 Q9CXV3 | Q9CXV3 mus musculu |
| 29 | 51 | 27.1 | 174 | 11 Q9CXK5 | Q9CXK5 mus musculu |
| 30 | 51 | 27.1 | 378 | 4 Q96H15 | Q96H15 homo sapien |
| 31 | 51 | 27.1 | 628 | 13 Q42455 | Q42455 raja eglant |
| 32 | 51 | 27.1 | 995 | 13 Q91638 | Q91638 xenopus lae |
| 33 | 51 | 27.1 | 1031 | 13 Q42124 | Q42124 gallus gall |
| 34 | 50.5 | 26.9 | 242 | 10 Q8S4L4 | Q8S4L4 lycopersico |
| 35 | 50.5 | 26.9 | 313 | 5 Q24330 | Q24330 dictyosteli |
| 36 | 50.5 | 26.9 | 397 | 10 Q8S4L3 | Q8S4L3 lycopersico |
| 37 | 50 | 26.6 | 467 | 10 Q49633 | Q49633 arabidopsis |
| 38 | 50 | 26.6 | 720 | 10 Q8H4W0 | Q8H4W0 oryza sativ |
| 39 | 50 | 26.6 | 8601 | 2 Q8GM87 | Q8GM87 symbiont ba |
| 40 | 49.5 | 26.3 | 330 | 10 Q946D5 | Q946D5 arabidopsis |
| 41 | 49.5 | 26.3 | 341 | 10 Q8L8P1 | Q8L8P1 arabidopsis |
| 42 | 49.5 | 26.3 | 343 | 10 Q9LUC1 | Q9LUC1 arabidopsis |
| 43 | 49.5 | 26.3 | 899 | 10 Q9SKI8 | Q9SKI8 arabidopsis |
| 44 | 49.5 | 26.3 | 902 | 10 Q9M364 | Q9M364 arabidopsis |
| 45 | 49.5 | 26.3 | 949 | 10 Q9XE44 | Q9XE44 arabidopsis |

ALIGNMENTS

RESULT 1

| | | | |
|--|--------------|------|---------|
| Q969J5 | PRELIMINARY; | PRT; | 263 AA. |
| ID Q969J5 | | | |
| AC Q969J5; | | | |
| DT 01-DEC-2001 (TrEMBLrel. 19, Created) | | | |
| DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) | | | |
| DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) | | | |
| DE Soluble cytokine class II receptor, long isoform precursor | | | |
| DE (Interleukin 22-binding protein CRF2-10L). | | | |
| GN CRF2-S1 OR IL22BP. | | | |
| OS Homo sapiens (Human). | | | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX NCBI_TaxID=9606; | | | |
| RN [1] | | | |
| RP SEQUENCE FROM N.A. | | | |
| RC TISSUE=Placenta; | | | |
| RX MEDLINE=21518574; PubMed=11607789; | | | |
| RA Gruenberg B.H., Schoenemeyer A., Weiss B., Toschi L., Kunz S., | | | |
| RA Wolk K., Asadullah K., Sabat R.; | | | |
| RT "A novel, soluble homologue of the human IL-10 receptor with | | | |
| RT preferential expression in placenta."; | | | |
| RL Genes Immun. 2:329-334 (2001). | | | |
| RN [2] | | | |
| RP SEQUENCE FROM N.A. | | | |
| RX MEDLINE=21286453; PubMed=11390454; | | | |
| RA Kotenko S.V., Izotova L.S., Mirochnitchenko O.V., Esterova E., | | | |
| RA Dickensheets H., Donnelly R.P., Pestka S.; | | | |
| RT "Identification, cloning, and characterization of a novel soluble | | | |
| RT receptor that binds IL-22 and neutralizes its activity."; | | | |
| RL J. Immunol. 166:7096-7103 (2001). | | | |
| DR EMBL; AJ313162; CAC85635.1; - | | | |
| DR EMBL; AY040567; AAK85715.1; - | | | |
| DR Genew; HGNC:14901; IL22RA2. | | | |
| DR InterPro; IPR000282; Cytok_receptor_2. | | | |
| FW Receptor; Signal. | | | |
| FT SIGNAL 1 21 POTENTIAL. | | | |
| FT CHAIN 22 263 SOLUBLE CYTOKINE CLASS II RECEPTOR, LONG | | | |
| FT ISOFORM. | | | |

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SQ SEQUENCE 263 AA; 30550 MW; C96CEC5D78AC79B CRC64;

Query Match 100.0%; Score 188; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFSCSMKSSHQKPSGCGWHISCNFPFGCRTLAK 32
| | | | | | | | | | | | | | | | | | | | | |
Db 67 MFSCSMKSSHQKPSGCGWHISCNFPFGCRTLAK 98

RESULT 2
Q8CX51
ID Q8CX51 PRELIMINARY; PRT; 367 AA.
AC Q8CX51
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative rhodanese-like protein.
GN LA3128.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011475; AAN50326.1; -.
KW Complete proteome.
SQ SEQUENCE 367 AA; 42467 MW; C1C1AA59DDF69785 CRC64;

Query Match 32.4%; Score 61; DB 16; Length 367;
Best Local Similarity 40.0%; Pred. No. 0.74;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 6 MKSSHQKPSGCGWHISCNFPFGCRTL 30
| | | | | | | | | | | | | | | | | | | | | |
Db 277 ISSCHQCGAKCDRHVNCNFCCHVL 301

RESULT 3
Q14230
ID Q14230 PRELIMINARY; PRT; 54 AA.
AC Q14230
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EHS-2 protein (Fragment).
GN EHS-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92194452; PubMed=1548756;
RA Horwitz M.S., Boyce-Jacino M.T., Faras A.J.;
RT "Novel human endogenous sequences related to human immunodeficiency
virus type 1."
RL J. Virol. 66:2170-2179 (1992).
DR EMBL; M86246; AAN58451.1; -.
FT NON TER 1
SQ SEQUENCE 54 AA; 6440 MW; AA56AF67667B3214 CRC64;

Query Match 31.6%; Score 59.5; DB 4; Length 54;
Best Local Similarity 52.2%; Pred. No. 0.19;
Matches 12; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

Qy 11 QKPSGCGWH-----ISCNFPFGCRTL 30
| | | | | | | | | | | | | | | | | | | | | |
Db 10 QAPSGCWQDSFCCSCSRINGCILL 32

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RESULT 4
Q8B121
ID Q8B121 PRELIMINARY; PRT; 515 AA.
AC Q8B121
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Glycoprotein precursor.
GN GPC.
OS Latino virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX NCBI_TaxID=45221;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Maru 10924;
RA Archer A.M.; Rico-Hesse R.;
RT "High Genetic Divergence and Recombination in Arenaviruses from the
Americas."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF485259; AAN09940.1; -.
SQ SEQUENCE 515 AA; 59232 MW; 9A247EC412383128 CRC64;

Query Match 31.1%; Score 58.5; DB 12; Length 515;
Best Local Similarity 40.0%; Pred. No. 2.4;
Matches 10; Conservative 3; Mismatches 5; Indels 7; Gaps 1;

Qy 4 CSMKSSHQKPSGCGWHISCNFPGCR 28
| | | | | | | | | | | | | | | | | | | | | |
Db 219 CQMGS DH-----QHICNYSNCK 236

RESULT 5
Q8B116
ID Q8B116 PRELIMINARY; PRT; 515 AA.
AC Q8B116
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Glycoprotein precursor.
OS Latino virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX NCBI_TaxID=45221;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MARU 10924;
RX MEDLINE=22197098; PubMed=12207889;
RA Charrel R.N.; Feldmann H.; Fulhorst C.F.; Khelifa R.; de Chesse R.;
RA de Lamballerie X.;
RT "Phylogeny of New World arenaviruses based on the complete coding
sequences of the small genomic segment identified an evolutionary
RT lineage produced by intrasegmental recombination."
RL Biochem. Biophys. Res. Commun. 296:1118-1124 (2002).
DR EMBL; AF512830; AAN32959.1; -.
SQ SEQUENCE 515 AA; 59222 MW; AA247F14123831B1 CRC64;

Query Match 31.1%; Score 58.5; DB 12; Length 515;
Best Local Similarity 40.0%; Pred. No. 2.4;
Matches 10; Conservative 3; Mismatches 5; Indels 7; Gaps 1;

Qy 4 CSMKSSHQKPSGCGWHISCNFPGCR 28
| | | | | | | | | | | | | | | | | | | | | |
Db 219 CQMGS DH-----QHICNYSNCK 236

RESULT 6
Q9CK78
ID Q9CK78 PRELIMINARY; PRT; 206 AA.
AC Q9CK78
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE DmsB.

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GN DMSB OR PM1755.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang O., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; A806212; AAK03839.1; -.
DR HSSP; P00195; 1CLF.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR000345; CytC_heme_bind.
DR Pfam; PF00037; fer4; 3.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 2.
KW Complete proteome.
SQ SEQUENCE 206 AA; 22901 MW; F3FE2DC10936EBFF CRC64;

Query Match 30.6%; Score 57.5; DB 16; Length 206;
Best Local Similarity 42.9%; Pred. No. 1.4;
Matches 12; Conservative 2; Mismatches 3; Indels 11; Gaps 2;

QY 11 QKPSGCMQH-----ISCNF---PGC 27
DB 49 QQANGCQHNHFAYLISLSCNHCNPNAC 76

RESULT 7
Q96AP5 PRELIMINARY; PRT; 383 AA.
ID Q96AP5
AC Q96AP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Lung;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016874; AAH16874.1; -.
DR InterPro; IPR001766; TF_Fork_head.
DR InterPro; IPR007087; ZnF_C2H2.
DR Pfam; PF00250; Fork_head; 1.
DR Pfam; PF00096; zf-C2H2; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR SMART; SM00355; ZnF_C2H2; 1.
DR PROSITE; PS00039; ZINC_FINGER_3; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 1.
KW Hypothetical protein; Metal-binding; zinc; Zinc-finger.
FT NON_TER 1
SQ SEQUENCE 383 AA; 42084 MW; 838CD68181AE2CCB CRC64;

Query Match 30.1%; Score 56.5; DB 4; Length 383;
Best Local Similarity 39.3%; Pred. No. 3.5;
Matches 11; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

QY 8 SSHQKPSG---CWOHISCNFPFGCRTLAK 32
DB 24 SSHEETPGSHPLYGHGCKWPGCETLCE 51

RESULT 8
Q96AP5 PRELIMINARY; PRT; 383 AA.
ID Q96AP5
AC Q96AP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Lung;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016874; AAH16874.1; -.
DR InterPro; IPR001766; TF_Fork_head.
DR InterPro; IPR007087; ZnF_C2H2.
DR Pfam; PF00250; Fork_head; 1.
DR Pfam; PF00096; zf-C2H2; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR SMART; SM00355; ZnF_C2H2; 1.
DR PROSITE; PS00039; ZINC_FINGER_3; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 1.
KW Hypothetical protein; Metal-binding; zinc; Zinc-finger.
FT NON_TER 1
SQ SEQUENCE 383 AA; 42084 MW; 838CD68181AE2CCB CRC64;

Query Match 30.1%; Score 56.5; DB 4; Length 383;
Best Local Similarity 39.3%; Pred. No. 3.5;
Matches 11; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

QY 8 SSHQKPSG---CWOHISCNFPFGCRTLAK 32
DB 24 SSHEETPGSHPLYGHGCKWPGCETLCE 51

RESULT 8
Q96AP5 PRELIMINARY; PRT; 383 AA.
ID Q96AP5
AC Q96AP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Lung;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016874; AAH16874.1; -.
DR InterPro; IPR001766; TF_Fork_head.
DR InterPro; IPR007087; ZnF_C2H2.
DR Pfam; PF00250; Fork_head; 1.
DR Pfam; PF00096; zf-C2H2; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR SMART; SM00355; ZnF_C2H2; 1.
DR PROSITE; PS00039; ZINC_FINGER_3; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 1.
KW Hypothetical protein; Metal-binding; zinc; Zinc-finger.
FT NON_TER 1
SQ SEQUENCE 383 AA; 42084 MW; 838CD68181AE2CCB CRC64;
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```
Q8IW55 PRELIMINARY; PRT; 667 AA.
ID Q8IW55
AC Q8IW55;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1200010K03 gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Skin;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040962; AAH40962.1; -.
DR EMBL; BC040962; AAH40962.1; -.
SQ SEQUENCE 667 AA; 72216 MW; 41ED0AF8996FE17F CRC64;

Query Match 30.1%; Score 56.5; DB 4; Length 667;
Best Local Similarity 39.3%; Pred. No. 6;
Matches 11; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

QY 8 SSHQKPSG---CWOHISCNFPFGCRTLAK 32
DB 291 SSHEETPGSHPLYGHGCKWPGCETLCE 318

RESULT 9
Q8IW55 PRELIMINARY; PRT; 680 AA.
ID Q8IW55
AC Q8IW55;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fork head-related protein like A.
GN HFKHLA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Daigo Y., Takayama I., Fujino M.A.;
RL "Isolation, mapping, and characterization of a novel human cDNA
RT differentially expressed in the fundus of W/Wv mutant mice.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080747; BAC53809.1; -.
DR EMBL; AB080747; BAC53809.1; -.
SQ SEQUENCE 680 AA; 73488 MW; A63826ED85B24752 CRC64;

Query Match 30.1%; Score 56.5; DB 4; Length 680;
Best Local Similarity 39.3%; Pred. No. 6.1;
Matches 11; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

QY 8 SSHQKPSG---CWOHISCNFPFGCRTLAK 32
DB 292 SSHEETPGSHPLYGHGCKWPGCETLCE 319

RESULT 10
Q8IW55 PRELIMINARY; PRT; 742 AA.
ID Q8IW55
AC Q8IW55;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Variant-specific surface protein AS10.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB;
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Query Match 29.3%; Score 55; DB 4; Length 320;
Best Local Similarity 50.0%; Pred. No. 4.9;
Matches 10; Conservative 5; Mismatches 5; Indels

Query Match 29.3%; Score 55; DB 4; Length 761;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 10; Conservative 5; Mismatches 5; Indels

QY 5 SMKSSHQPSGCWQHISCNF 24
|::|||::| |::|

Db 19 SVQPSHQEPACTDQHSKEF 38

RESULT 15

Q90XF6 PRELIMINARY; PRT; 367 AA.
AC Q90XF6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Zinc finger buttonhead-related transcription factor 1.
GN BSL1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21521131; PubMed=11641225;
RA Tallafuss A., Wilm T.P., Crozatier M., Pfeffer P., Wassef M.,
RA Bally-Cuif L.;
RT "The zebrafish buttonhead-like factor Bsl1 is an early regulator of
RT pax2.1 expression during mid-hindbrain development.";
RL Development 128:4021-4034(2001).
DR EMBL; AF388363; AAK83353.1; -.
DR InterPro; IPR07087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2_3.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 367 AA; 41030 MW; F31946B6A66CD8FD CRC64;
QY 3 SCMSKSHQKPSGCGWHISCNFPQC 27
Db 246 NCOSSSSDEFGKKQHI-CHIPQC 269

Query Match 29.0%; Score 54.5; DB 13; Length 367;
Best Local Similarity 44.0%; Pred. No. 6.6;
Matches 11; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Search completed: December 12, 2003, 12:27:22
Job time : 8.61695 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 12:16:38 ; Search time 2.06102 Seconds
(without alignments)
730.151 Million cell updates/sec

Title: US-10-047-264a-4_COPY_67_98

Perfect score: 188

Sequence: 1 MFSCSKSHQKPCSCWQHISCNFFGCRFLAK 32

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 61 | 32.4 | 367 | 1 YV28 LEPIN | O8CXSL leptospira |
| 2 | 51 | 27.1 | 158 | 1 CRGF_MOUSE | Q03740 mus musculus |
| 3 | 51 | 27.1 | 173 | 1 CRGD_MOUSE | P04342 mus musculus |
| 4 | 51 | 27.1 | 173 | 1 CRGD_RAT | P10067 rattus norv |
| 5 | 51 | 27.1 | 173 | 1 CRGE_MOUSE | P26999 mus musculus |
| 6 | 51 | 27.1 | 173 | 1 CRGE_RAT | P02528 rattus norv |
| 7 | 51 | 27.1 | 173 | 1 CRGF_RAT | P10068 rattus norv |
| 8 | 50 | 26.6 | 88 | 1 CX9A_CONGL | Q9GU57 conus glori |
| 9 | 49.5 | 26.3 | 266 | 1 YXKA_CABEL | Q95GY7 caenorhabdi |
| 10 | 49 | 26.1 | 126 | 1 CD59_PAPSP | Q28785 papio sp. (|
| 11 | 49 | 26.1 | 128 | 1 CD59_CERAE | Q28216 cercopithec |
| 12 | 49 | 26.1 | 851 | 1 NCL1_CABEL | P34611 caenorhabdi |
| 13 | 48 | 25.5 | 88 | 1 CX9A_CONTE | Q9GU58 conus texti |
| 14 | 48 | 25.5 | 365 | 1 P43_XENLA | P25456 xenopus lae |
| 15 | 48 | 25.5 | 593 | 1 GRN_HUMAN | P28799 h granulins |
| 16 | 48 | 25.5 | 597 | 1 ZF37_HUMAN | Q9Y6Q3 homo sapien |
| 17 | 48 | 25.5 | 633 | 1 ACES_ELEBL | O42275 electrophor |
| 18 | 47.5 | 25.3 | 246 | 1 BONF_CHICK | P25429 gallus gall |
| 19 | 47.5 | 25.3 | 747 | 1 YU20_MOUSE | Q9WV70 mus musculu |
| 20 | 47.5 | 25.3 | 806 | 1 TRAI_MAIZE | P08770 zea mays (m |
| 21 | 47.5 | 25.3 | 836 | 1 TRAI_MAIZE | P03010 zea mays (m |
| 22 | 47 | 25.0 | 167 | 1 RT25_DROME | Q9YV28 drosophila |
| 23 | 47 | 25.0 | 519 | 1 YMP4_YEAST | O04347 saccharomyc |
| 24 | 47 | 25.0 | 759 | 1 CAS1_ARATH | P38605 arabidopsis |
| 25 | 47 | 25.0 | 1247 | 1 POLS_ONNVG | P22056 o'nyong-nyo |
| 26 | 47 | 25.0 | 2038 | 1 FSH_DROME | P13709 drosophila |
| 27 | 46.5 | 24.7 | 150 | 1 YHE2_YEAST | P38729 saccharomyc |
| 28 | 46.5 | 24.7 | 408 | 1 IHH_CHICK | Q98938 gallus gall |
| 29 | 46 | 24.5 | 51 | 1 AF2A_SINAL | P30232 sinapis alb |
| 30 | 46 | 24.5 | 340 | 1 CATB_CHICK | P43233 gallus gall |
| 31 | 46 | 24.5 | 611 | 1 AFAM_MOUSE | O89020 mus musculu |
| 32 | 46 | 24.5 | 670 | 1 NKX2_RAT | O54701 rattus norv |
| 33 | 46 | 24.5 | 749 | 1 YU20_HUMAN | Q9Y3T9 homo sapien |

Q05895 mus musculu
P03315 semliki for
P08491 ross river
Q16227 aedes aegypt
O05083 haemophilus
Q63514 rattus norv
P03083 polyomaviru
Q07394 rhodobacter
O42506 fugu rubrip
P89116 spodoptera
Q09150 schizosacch
Q8ZQ23 salmonella

ALIGNMENTS

RESULT 1
YV28 LEPIN
ID YV28 LEPIN STANDARD; PRT; 367 AA.
AC Q8CXSL;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein LA3128.
GN LA3128.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
CC -!- SIMILARITY: BELONGS TO THE UPF0176 FAMILY.
CC -!- SIMILARITY: Contains 1 rhodanese domain.
CC
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CC
CC -----
CC HAWAP; AE011475; AAN50326.1; -.
DR HAWAP; MF 00469; -; 1
DR Pfam; PF00581; Rhodanese; 1.
DR SMART; SM00450; RHOD; 1.
DR PROSITE; PS0206; RHODANES_3; 1.
DR PROSITE; PS0206; RHODANES_3; 1.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 159 253 RHODANES.
SQ SEQUENCE 367 AA; 42467 MW; C1CIAA59DDPF69785 CRC64;
Query Match 32.4%; Score 61; DB 1; Length 367;
Best Local Similarity 40.0%; Pred. No. 0.69;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 6 MKSSHQKPCSCWQHISCNFFGCRFL 30
Db 277 ISSCHQCGAKCDHRVNCNFCGCHVL 301

RESULT 2


```
AC P10067;
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Gamma crystallin D (Gamma crystallin 2-2).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90236314; PubMed=1970548;
RA den Dunnen J.T., van Neck J.W., Cremers F.P.M., Lubsen N.H.,
RA Schoenmakers J.G.G.;
RT "Isolation and characterization of the rat glutamine
RT synthetase-encoding gene.";
RL Gene 87:225-232(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87060933; PubMed=3783678;
RA den Dunnen J.T., Moormann R.J.M., Lubsen N.H., Schoenmakers J.G.G.;
RA "Concerted and divergent evolution within the rat gamma-crystallin
RT gene family.";
RL J. Mol. Biol. 189:37-46(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lens;
RX MEDLINE=95151850; PubMed=7849105;
RA Ooki K., Amuro N., Shimizu Y., Okazaki T.;
RA "High level expression of rat gamma-D-crystallin in Escherichia
RT coli.";
RL Biochimie 76:398-403(1994).
CC -!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -!- MISCELLANEOUS: THERE ARE SIX DIFFERENT GAMMA CRYSTALLINS
CC IDENTIFIED IN RAT LENS.
CC -!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
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CC
CC EMBL; M19359; AAA40984.1; -.
CC FIR; D24060; D24060.
CC HSSP; P02528; 1A5D.
CC InterPro; IPR001064; Crystallin.
CC Pfam; PF00030; crystall; 2.
CC PRINTS; PR01367; BGCYSTALLIN.
CC SMART; SM00247; XTALbg; 2.
CC PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 4.
CC Eye lens protein; Multigene family; Repeat.
CC INIT MET 0 0
CC FT DOMAIN 1 39 MOTIF 1.
CC FT DOMAIN 40 83 MOTIF 2.
CC FT DOMAIN 84 86 CONNECTING PEPTIDE.
CC FT DOMAIN 87 127 MOTIF 3.
CC FT DOMAIN 128 173 MOTIF 4.
CC SQ SEQUENCE 173 AA; 20972 MW; 930B2D42D80F4117 CRC64;
Query Match 27.1%; Score 51; DB 1; Length 173;
Best Local Similarity 30.8%; Pred. No. 6.8;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;
QY 2 FSCMKSSHQKP-----SGCWQ-HISCNFPGCR 28
DB 16 YECSTHSLNLPYFRCNSVRVDSGCMWLYEQPNFTGCQ 54
```

```
RESULT 5
CRGE_MOUSE STANDARD; PRT; 173 AA.
ID CRGE_MOUSE
AC P26999;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Gamma crystallin E.
GN CRYGE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=(101/Elx3H/El)F1; TISSUE=Liver;
RX MEDLINE=92009223; PubMed=1916296;
RA Graw J., Coban L., Liebshtein A., Werner T.;
RA "Murine gamma E-crystallin is distinct from murine gamma
RT 2-crystallin".
RL Gene 104:265-270(1991).
CC -!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -!- MISCELLANEOUS: THERE ARE SIX DIFFERENT GAMMA CRYSTALLINS
CC IDENTIFIED IN MOUSE LENS.
CC -!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
CC
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CC
CC EMBL; X57855; CAA40990.1; -.
CC FIR; S26811; S26811.
CC HSSP; P02528; 1A5D.
CC MGD; MGI:88525; Cryge.
CC InterPro; IPR001064; Crystallin.
CC Pfam; PF00030; crystall; 2.
CC PRINTS; PR01367; BGCYSTALLIN.
CC SMART; SM00247; XTALbg; 2.
CC PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 4.
CC Eye lens protein; Multigene family; Repeat.
CC INIT MET 0 0
CC FT DOMAIN 1 39 MOTIF 1.
CC FT DOMAIN 40 83 MOTIF 2.
CC FT DOMAIN 84 86 CONNECTING PEPTIDE.
CC FT DOMAIN 87 127 MOTIF 3.
CC FT DOMAIN 128 173 MOTIF 4.
CC SQ SEQUENCE 173 AA; 21093 MW; E17410F82B3C39AE CRC64;
Query Match 27.1%; Score 51; DB 1; Length 173;
Best Local Similarity 30.8%; Pred. No. 6.8;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;
QY 2 FSCMKSSHQKP-----SGCWQ-HISCNFPGCR 28
DB 16 YECSTHSLNLPYFRCNSVRVDSGCMWLYEQPNFTGCQ 54
```

DE Gamma crystallin E (Gamma crystallin 3-1) (Gamma-2).
OS Rattus norvegicus (Rat), and
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116, 10090;
RN (1)
RP SEQUENCE FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=90236314; PubMed=1970548;
RA den Dunnen J.T., van Neck J.W., Cremers F.P.M., Lubsen N.H.,
RA Schoenmakers J.G.G.;
RT "Isolation and characterization of the rat glutamine
RT synthetase-encoding gene.";
RL Gene 87:225-232(1990).
RN (2)
RP SEQUENCE FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=83091061; PubMed=6294661;
RA Moormann R.J.M., den Dunnen J.T., Bloemendal H.,
RA Schoenmakers J.G.G.;
RT "Extensive intragenic sequence homology in two distinct rat lens
RT gamma-crystallin cDNAs suggests duplications of a primordial gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6876-6880(1982).
RN (3)
RP SEQUENCE FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=84114867; PubMed=6319707;
RA Moormann R.J.M., den Dunnen J.T., Mulleners L., Andreoli P.,
RA Bloemendal H., Schoenmakers J.G.G.;
RT "Strict co-linearity of genetic and protein folding domains in an
RT intragenically duplicated rat lens gamma-crystallin gene.";
RL J. Mol. Biol. 171:353-368(1983).
RN (4)
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=85088487; PubMed=6096855;
RA Breitman M.L., Lok S., Wistow G., Piatigorsky J., Treton J.A.,
RA Gold R.J.M., Tsui L.C.;
RT "Gamma-crystallin family of the mouse lens: structural and
RT evolutionary relationships.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:7762-7766(1984).
RN (5)
RP SEQUENCE OF 1-68 FROM N.A.
RC SPECIES=Mouse; TISSUE=Lens;
RX MEDLINE=86284663; PubMed=3837188;
RA Lok S., Breitman M.L., Chepelinsky A.B., Piatigorsky J.,
RA Gold R.J.M., Tsui L.C.;
RT "Lens-specific promoter activity of a mouse gamma-crystallin gene.";
RL Mol. Cell. Biol. 5:2221-2230(1985).
RN (6)
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC SPECIES=Rat; TISSUE=Lens;
RX MEDLINE=98035705; PubMed=9367641;
RA Norledge B.V., Hay R.E., Bateman O.A., Slingsby C., Driessen H.P.C.;
RT "Towards a molecular understanding of phase separation in the lens: a
RT comparison of the X-ray structures of two high Tc gamma-crystallins,
RT gammaE and gammaF, with two low Tc gamma-crystallins, gammaB and
RT gammaD.";
RL Exp. Eye Res. 65:609-630(1997).
CC -1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST SEVEN DIFFERENT GAMMA
CC CRYSTALLINS IDENTIFIED IN MOUSE LENS.
CC -1- MISCELLANEOUS: THERE ARE SIX DIFFERENT GAMMA CRYSTALLINS
CC IDENTIFIED IN RAT LENS.
CC -1- MISCELLANEOUS: THE TWO SEQUENCES SEEM IDENTICAL. WHAT IS KNOWN AS
CC GAMMA-E IN RAT IS CALLED GAMMA-2 IN MOUSE. THERE IS ANOTHER
CC GAMMA-E SEQUENCE IN MOUSE.
CC -1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M19359; AAA40985.1; -;
DR EMBL; J00716; AAA40987.1; -;
DR EMBL; X00271; CAA25073.1; -;
DR EMBL; K02584; AAA03228.1; -;
DR EMBL; M11039; AAA03227.1; -;
DR PIR; A02930; CVRTGL;
DR PIR; A02931; CYMSG2;
DR PIR; I56381; I56381.
DR PDB; 1ASD; 27-MAY-98.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00303; crystall; 2.
DR PRINTS; PR01367; BGCYSTALLIN.
DR SMART; SM00247; XTALBgl; 2.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 4.
KW Eye lens protein; Multigene family; Repeat; 3D-structure.
FT INIT MET 0 0
FT DOMAIN 1 39 MOTIF 1.
FT DOMAIN 40 83 MOTIF 2.
FT DOMAIN 84 86 CONNECTING PEPTIDE.
FT DOMAIN 87 127 MOTIF 3.
FT DOMAIN 128 173 MOTIF 4.
FT STRAND 2 8
FT TURN 9 11
FT STRAND 12 18
FT STRAND 22 22
FT HELIX 26 28
FT STRAND 34 39
FT TURN 41 47
FT STRAND 48 50
FT STRAND 51 57
FT STRAND 60 62
FT HELIX 65 68
FT TURN 69 69
FT STRAND 77 81
FT STRAND 88 92
FT HELIX 95 97
FT STRAND 101 104
FT STRAND 108 108
FT HELIX 111 114
FT STRAND 122 127
FT STRAND 130 135
FT TURN 136 138
FT STRAND 139 145
FT STRAND 148 150
FT HELIX 153 156
FT TURN 157 157
FT STRAND 165 168
SQ SEQUENCE 173 AA; 21132 MW; 3F3200E85CB61B02 CRC64;
Query Match 27.4%; Score 51; DB 1; Length 173;
Best Local Similarity 30.8%; Pred. No. 6.8;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;
Oy 2 FSCSMKSSHOKP-----SGCWQ-HISCNFPCCR 28
Db 16 YECSTHSLQPYFSCNCSVRVDSGCMWLYEQPNFTGCQ 54
RESULT 7
CRGF_RAT STANDARD; PRT; 173 AA.
ID CRGF_RAT
AC P10068;
DC 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Gamma crystallin P (Gamma crystallin 4-1).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87060933; PubMed=3783678;
 RA den Dunnen J.T., Moormann R.J.M., Lubsen N.H., Schoenmakers J.G.G.;
 RT "Concerted and divergent evolution within the rat gamma-crystallin
 gene family.";
 RL J. Mol. Biol. 189:37-46(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90236314; PubMed=1970548;
 RA den Dunnen J.T., van Neck J.W., Cremers F.P.M., Lubsen N.H.,
 RA Schoenmakers J.G.G.;
 RT "Isolation and characterization of the rat glutamine
 synthetase-encoding gene.";
 RL Gene 87:225-232(1990).
 CC -|- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
 OF THE VERTEBRATE EYE LENS.
 CC -|- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
 VERY SIMILAR GREEK KEY MOTIFS.
 CC -|- MISCELLANEOUS: THERE ARE SIX DIFFERENT GAMMA CRYSTALLINS
 IDENTIFIED IN RAT LENS.
 CC -|- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
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 DR EMBL; M19357; AAA40988.1; -;
 DR FIR; E24060; E24060.
 DR HSP; P02528; IASD.
 DR InterPro; IPR001064; Crystallin.
 DR Pfam; PF00030; Crystallin; 2.
 DR PRINTS; PR01367; BGCYSTALLIN.
 DR SMART; SM00247; XTALPG; 2.
 DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 4.
 KW Eye lens protein; Multigene family; Repeat.
 FT INIT MET 0 0
 FT DOMAIN 1 39 MOTIF 1.
 FT DOMAIN 40 83 MOTIF 2.
 FT DOMAIN 84 86 CONNECTING PEPTIDE.
 FT DOMAIN 87 127 MOTIF 3.
 FT DOMAIN 128 173 MOTIF 4.
 SQ SEQUENCE 173 AA; 21210 MW; 40B63B99F75600BD CRC64;
 Query Match 27.1%; Score 51; DB 1; Length 173;
 Best Local Similarity 30.8%; Pred. No. 6.8;
 Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;
 QY 2 FSCSMKSHQKP-----SCWQ-HISCNFPGCR 28
 DB 16 YECSTDHNLQYFRCNSVRVDSGCMWLYEQPNFTGQ 54
 RESULT 8
 CX9A_CONGL STANDARD; PRT; 88 AA.
 AC Q9GU57;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Spasmodic protein t9a-like protein precursor (Conotoxin Gm9.1).
 OS Conus gloriarius (Glory of the sea).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbecoconcha; Hypogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=37336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20143473; PubMed=10677206;
 RA Lirazan M.B., Hooper D., Corpuz G.P., Ramilo C.A., Bandyopadhyay P.,
 RA Cruz L.J., Olivera B.M.;
 RT "The spasmodic peptide defines a new conotoxin superfamily.";
 RL Biochemistry 39:1583-1588(2000)
 CC -|- FUNCTION: Not known. Has only been studied at nucleotide level.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -|- SIMILARITY: BELONGS TO THE P-SUPERFAMILY OF CONOTOXINS.
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 DR EMBL; AF193511; AAG28407.1; -;
 DR PDB; 1IXT; 28-JAN-03.
 KW Toxin; Signal; Amidation; Cleavage on pair of basic residues;
 KW 3D-structure.
 FT SIGNAL 1 27 POTENTIAL.
 FT PROPEP 28 60 PROBABLE.
 FT PEPTIDE 61 87 SPASMODIC PROTEIN TX9A-LIKE PROTEIN.
 FT DISULFID 62 76 PROBABLE.
 FT DISULFID 66 78 PROBABLE.
 FT DISULFID 72 83 PROBABLE.
 FT MOD_RES 87 87 AMIDATION (G-88 PROVIDE AMIDE GROUP)
 FT SEQUENCE 88 AA; 9687 MW; C82818A55C8C44E7 CRC64;
 Query Match 26.6%; Score 50; DB 1; Length 88;
 Best Local Similarity 43.5%; Pred. No. 4.9;
 Matches 10; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
 QY 5 SMKSHQKPSGCGWHISCNFPGC 27
 DB 61 SCNNSCQSHDCASHCICITFRGC 83
 RESULT 9
 YKKA_CAEEL STANDARD; PRT; 266 AA.
 AC Q95QY7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hypothetical zinc finger protein C02F5.12 in chromosome III.
 GN C02F5.12.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA LaReille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkhen R.,
 RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Woldman P.;

RC TISSUE=Brain;
RA Yu W., Gibbs R.A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Cervix, and lung;
RX MEDLINE=2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Hsieh F.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Stapchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RP SEQUENCE OF 206-233; 281-336; 364-396 AND 442-447.
RC TISSUE=Leukocyte;
RX MEDLINE=91097544; PubMed=2268320;
RA Bateman A., Belcourt D.R., Bennett H.P., Lazure C., Solomon S.;
RT "Granulins, a novel class of peptide from leukocytes.";
RL Biochem. Biophys. Res. Commun. 173:1161-1168 (1990).
CC -!- FUNCTION: GRANULINS HAVE POSSIBLE CYTOKINE-LIKE ACTIVITY. THEY MAY
CC PLAY A ROLE IN INFLAMMATION, WOUND REPAIR, AND TISSUE REMODELING.
CC -!- FUNCTION: GRANULIN A PROMOTES PROLIFERATION OF THE EPITHELIAL CELL
CC LINE A431 IN CULTURE WHILE GRANULIN B ACTS AS AN ANTAGONIST TO
CC GRANULIN A. INHIBITING THE GROWTH.
CC GRANULIN A. INHIBITING THE GROWTH.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P28799-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P28799-2; Sequence=VSP_001837;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: IN MYELOGENOUS LEUKEMIC CELL LINES OF
CC PROMONOCYTIC, PROMYELOCYTIC, AND PROERYTHROID LINEAGE, IN
CC FIBROBLASTS, AND VERY STRONGLY IN EPITHELIAL CELL LINES. PRESENT
CC IN INFLAMMATORY CELLS AND BONE MARROW. HIGHEST LEVELS IN KIDNEY.
CC -!- PTM: GRANULINS ARE DISULFIDE BRIDGED.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M75161; AAA58617.1; ALT_SEQ.
CC EMBL; X62320; CRA4196.1; -.
CC EMBL; AF055008; AAC09359.1; -.
CC EMBL; BC000324; AAH00324.1; -.
CC EMBL; BC010577; AAH10577.1; -.
CC PIR; JC1284; GYHU.
CC PDB; 1G26; 01-NOV-00.
CC Genew; HGNC:4601; GRN.
CC MIM; 138945; -.
CC GO; GO:0008083; F: growth factor activity; TAS.
CC InterPro; IPR000118; Granulin.
CC Pfam; PF00396; granulin; 7.
CC SMART; SM00277; GRAN; 7.

DR PROSITE; PS00799; GRANULINS; 7.
KW Cytokine; Repeat; Glycoprotein; Signal; Alternative splicing;
KW Polymorphism; 3D-structure.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 593 ACROGRANIN.
FT PEPTIDE 18 747 PARAGRANULIN.
FT PEPTIDE 758 7113 GRANULIN 1.
FT PEPTIDE 7123 7179 GRANULIN 2.
FT PEPTIDE 206 261 GRANULIN 3.
FT PEPTIDE 281 336 GRANULIN 4.
FT PEPTIDE 364 7417 GRANULIN 5.
FT PEPTIDE 442 7496 GRANULIN 6.
FT PEPTIDE 7518 7573 GRANULIN 7.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 530 530 Missing (in isoform 2).
FT VARSPLIT 377 531 /FTid=VSP_001837.
FT VARIANT 454 454 G -> Q.
FT VARIANT 515 515 /FTid=VAR_003445.
FT VARIANT 219 219 G -> A (IN dbSNP:25647).
FT CONFLICT 219 219 S -> H (IN REF. 6).
FT CONFLICT 386 386 W -> H (IN REF. 6).
FT SEQUENCE 593 AA; 63473 MW; 4E402BDB16DE2819 CRC64;
Qy 9 SHQKPSGCGWOHISCNFPQ--CRTLL 30
Db 437 SHPRDIGCDQHTSCPVGGTCPSL 460
Query Match 25.5%; Score 48; DB 1; Length 593;
Best Local Similarity 45.8%; Pred. No. 52;
Matches 11; Conservative 2; Mismatches 9; Indels 2; Gaps 1;
Search completed: December 12, 2003, 12:26:07
Job time : 3.06102 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 12:07:47 ; Search time 3.14576 Seconds
(without alignments)
430.404 Million cell updates/sec

Title: US-10-047-264A-4_COPY_67_98

Perfect score: 188

Sequence: 1 MFSCMSKSHQKPSGCMQHSCNFGPCRTILAK 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A COMB pep.*
- 2: /cgn2_6/prodata/1/iaa/5B COMB pep.*
- 3: /cgn2_6/prodata/1/iaa/6A COMB pep.*
- 4: /cgn2_6/prodata/1/iaa/6B COMB pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS COMB pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 52 | 27.7 | 516 | 4 | US-09-252-991A-19788 |
| 2 | 49 | 26.1 | 163 | 2 | US-08-727-688-25 |
| 3 | 49 | 26.1 | 236 | 4 | US-09-252-991A-27618 |
| 4 | 49 | 26.1 | 515 | 4 | US-09-635-872A-6 |
| 5 | 49 | 26.1 | 515 | 4 | US-09-836-077A-6 |
| 6 | 48.5 | 25.8 | 365 | 4 | US-09-252-991A-30166 |
| 7 | 48 | 25.5 | 162 | 4 | US-09-252-991A-32591 |
| 8 | 48 | 25.5 | 297 | 4 | US-09-252-991A-28842 |
| 9 | 47.5 | 25.3 | 451 | 4 | US-09-252-991A-32664 |
| 10 | 47 | 25.0 | 27 | 4 | US-09-136-769A-4 |
| 11 | 47 | 25.0 | 27 | 4 | US-09-136-769A-15 |
| 12 | 47 | 25.0 | 67 | 1 | US-08-435-040-3 |
| 13 | 47 | 25.0 | 67 | 3 | US-09-020-216-3 |
| 14 | 47 | 25.0 | 144 | 4 | US-09-252-991A-31815 |
| 15 | 47 | 25.0 | 339 | 4 | US-09-252-991A-25235 |
| 16 | 47 | 25.0 | 533 | 4 | US-08-991-862-17 |
| 17 | 46.5 | 24.7 | 66 | 2 | US-08-511-485-24 |
| 18 | 46.5 | 24.7 | 66 | 4 | US-09-201-936-24 |
| 19 | 46.5 | 24.7 | 496 | 2 | US-08-511-485-10 |
| 20 | 46.5 | 24.7 | 496 | 3 | US-09-212-971-10 |
| 21 | 46.5 | 24.7 | 496 | 3 | US-08-800-829A-10 |
| 22 | 46.5 | 24.7 | 496 | 4 | US-09-617-053A-10 |
| 23 | 46.5 | 24.7 | 496 | 4 | US-09-201-936-10 |
| 24 | 46 | 24.5 | 26 | 1 | US-08-377-687-8 |
| 25 | 46 | 24.5 | 26 | 2 | US-08-777-192-8 |
| 26 | 46 | 24.5 | 26 | 3 | US-08-971-982-8 |
| 27 | 46 | 24.5 | 26 | 4 | US-09-077-951-17 |

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| 28 | 46 | 24.5 | 154 | 4 | US-09-252-991A-25612 | Sequence 25612, A |
| 29 | 46 | 24.5 | 173 | 4 | US-09-252-991A-30903 | Sequence 30903, A |
| 30 | 46 | 24.5 | 232 | 4 | US-09-252-991A-23648 | Sequence 23648, A |
| 31 | 46 | 24.5 | 160 | 4 | US-09-252-991A-32452 | Sequence 32452, A |
| 32 | 46 | 24.5 | 445 | 4 | US-09-252-991A-24354 | Sequence 24354, A |
| 33 | 46 | 24.5 | 501 | 1 | US-08-722-001-14 | Sequence 14, Appl |
| 34 | 46 | 24.5 | 501 | 2 | US-08-467-568-9 | Sequence 9, Appl |
| 35 | 46 | 24.5 | 501 | 2 | US-09-030-582-9 | Sequence 9, Appl |
| 36 | 46 | 24.5 | 501 | 4 | US-09-688-415-7 | Sequence 7, Appl |
| 37 | 46 | 24.5 | 589 | 4 | US-09-252-991A-18009 | Sequence 18009, A |
| 38 | 46 | 24.5 | 593 | 1 | US-07-668-648-4 | Sequence 4, Appl |
| 39 | 46 | 24.5 | 593 | 2 | US-08-429-998-4 | Sequence 4, Appl |
| 40 | 46 | 24.5 | 593 | 2 | US-08-431-333-4 | Sequence 4, Appl |
| 41 | 46 | 24.5 | 593 | 5 | PCT-US91-02321-4 | Sequence 4, Appl |
| 42 | 46 | 24.5 | 947 | 4 | US-09-252-991A-21398 | Sequence 21398, A |
| 43 | 46 | 24.5 | 1253 | 1 | US-07-920-281C-3 | Sequence 3, Appl |
| 44 | 46 | 24.5 | 1253 | 3 | US-08-466-277-3 | Sequence 3, Appl |
| 45 | 45.5 | 24.2 | 349 | 4 | US-09-252-991A-17840 | Sequence 17840, A |

ALIGNMENTS

RESULT 1

US-09-252-991A-19788
; Sequence 19788, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19788
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19788

Query Match 27.7%; Score 52; DB 4; Length 516;
Best Local Similarity 36.6%; Pred. No. 20;
Matches 15; Conservative 3; Mismatches 7; Indels 16; Gaps 3;

QY 3 SCMSKSHQKPSGC-WQHIS-----CNFPGCRTLTA 31
Db 424 TCSPRS----PFCRWKPSAAWRSPAPRCPNCPGCTSYA 460

RESULT 2

US-08-727-688-25
; Sequence 25, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road D377/AP6D
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION NUMBER: US/08/727,688
; PRIOR APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5967.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 937-0378
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5919638e
; US-08-727-688-25

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Query Match      26.1%; Score 49; DB 2; Length 163;
Best Local Similarity 40.9%; Pred. No. 15;
Matches 9; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

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Qy 4 CSMKSSHQKPSGCWQHISCNFP 25
Db 72 CSSSSSCSWPTSCWS--TCSLP 91

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RESULT 3

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US-09-252-991A-27618
; Sequence 27618, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27618
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27618

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Query Match      26.1%; Score 49; DB 4; Length 236;
Best Local Similarity 36.4%; Pred. No. 22;
Matches 12; Conservative 5; Mismatches 8; Indels 8; Gaps 2;

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Qy 3 SCMSKSSHQ-----KPSGCWQHISCNFP 29
Db 3 SASAKSAHRATSAWNSAGCTARVSC--VSCRT 33

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RESULT 4

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US-09-635-872A-6
; Sequence 6, Application US/09635872A
; Patent No. 6534300
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYOSOMAL HYDROLASES
; FILE REFERENCE: 195613US0

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; CURRENT APPLICATION NUMBER: US/09/635,872A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(24)
; NAME/KEY: PROPEP
; LOCATION: (25)..(49)
; US-09-635-872A-6

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Query Match      26.1%; Score 49; DB 4; Length 515;
Best Local Similarity 56.2%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 13 PSCWQHISCNFP 28
Db 364 PSNCQHGCLCTGTGCR 379

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RESULT 5

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US-09-636-077A-6
; Sequence 6, Application US/09636077A
; Patent No. 6537785
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, WILLIAM
; TITLE OF INVENTION: METHODS OF TREATING LYOSOMAL STORAGE DISEASE
; FILE REFERENCE: 195612US0
; CURRENT APPLICATION NUMBER: US/09/636,077A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/153,831
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(24)
; NAME/KEY: PROPEP
; LOCATION: (25)..(49)
; US-09-636-077A-6

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Query Match      26.1%; Score 49; DB 4; Length 515;
Best Local Similarity 56.2%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 13 PSCWQHISCNFP 28
Db 364 PSNCQHGCLCTGTGCR 379

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RESULT 6

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US-09-252-991A-30166
; Sequence 30166, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

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|-----------------------|-------|---------------|-------|-------------|
| Query Match | 25.5% | Score 48; | DB 4; | Length 297; |
| Best Local Similarity | 37.5% | Pred. No. 39; | | |

Query Match 25.5%; Score 48; DB 4; Length 297;
Best Local Similarity 37.5%; Pred. No. 39;

Query Match 25.0%; Score 47; DB 4; Length 27;

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Best Local Similarity 45.0%; Pred. No. 4;
Matches 9; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 8 SSHQKPSGCMQHISCNFPGC 27
Db 4 NSCXHSDCXSHCTC1FRGC 23

RESULT 11
US-09-136-769A-15
; Sequence 15, Application US/09136769A
; Patent No. 6307014
; GENERAL INFORMATION:
; APPLICANT: Furlie, Bruce
; APPLICANT: Furlie, Barbara
; APPLICANT: Stenflo, Johan
; APPLICANT: Rigby, Alan C.
; APPLICANT: Roepstoft, Peter
; TITLE OF INVENTION: CONOPEPTIDES
; FILE REFERENCE: 50065/002001
; CURRENT APPLICATION NUMBER: US/09/136,769A
; CURRENT FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus textile
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (8)...(13)
; OTHER INFORMATION: Each Xaa is gamma-carboxyglutamic acid.
; NAME/KEY: VARIANT
; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: VARIANT
; LOCATION: (1)...(27)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-136-769A-15

Query Match 25.0%; Score 47; DB 4; Length 27;
Best Local Similarity 45.0%; Pred. No. 4;
Matches 9; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 8 SSHQKPSGCMQHISCNFPGC 27
Db 4 NSCXHSDCXSHCTC1FRGC 23

RESULT 12
US-08-435-040-3
; Sequence 3, Application US/08435040
; Patent No. 5756340
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Moskowitz, Haim
; TITLE OF INVENTION: Insect Control With Multiple Toxins
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,040

Qy 8 SSHQKPSGCMQHISCNFPGC 27
Db 4 NSCXHSDCXSHCTC1FRGC 23

RESULT 13
US-09-020-216-3
; Sequence 3, Application US/09020216
; Patent No. 6162430
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Moskowitz, Haim
; TITLE OF INVENTION: Insect Control With Multiple Toxins
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,216
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,040
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2500.078USO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

Qy 12 KPSGCMQHISCNFPGCRTLAK 32
Db 9 QPENCVYHCFPGSGCDTLCK 29

Query Match 25.0%; Score 47; DB 1; Length 67;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 12 KPSGCMQHISCNFPGCRTLAK 32
Db 9 QPENCVYHCFPGSGCDTLCK 29

US-08-435-040-3
; Sequence 3, Application US/09020216
; Patent No. 6162430
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Moskowitz, Haim
; TITLE OF INVENTION: Insect Control With Multiple Toxins
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,216
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,040
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2500.078USO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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Query Match      25.0%; Score 47; DB 4; Length 339;
Best Local Similarity 32.6%; Pred. No. 63;
Matches 14; Conservative 2; Mismatches 13; Indels 14; Gaps 2;

QY      3 SCSMKSSHOK-----PSGCW-----QHISCNPPGCTLA 31
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2003, 12:23:03 ; Search time 2.92881 Seconds
(without alignments)
1050.732 Million cell updates/sec

Title: US-10-047-264A-4_COPY_67_98

Perfect score: 188
Sequence: 1 MFSCMSKSHQPSGQWQHISCNFFGCRTLAK 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 59.5 | 31.6 | 54 | 2 | I74320 |
| 2 | 55 | 29.3 | 761 | 2 | gene EHS-2 protein |
| 3 | 51 | 27.1 | 69 | 2 | hypothetical prote |
| 4 | 51 | 27.1 | 159 | 2 | gamma-F-crystallin |
| 5 | 51 | 27.1 | 173 | 1 | gamma-P-crystallin |
| 6 | 51 | 27.1 | 173 | 2 | gamma-crystallin 1 |
| 7 | 51 | 27.1 | 174 | 1 | gamma-crystallin 2 |
| 8 | 51 | 27.1 | 174 | 1 | gamma-crystallin 1 |
| 9 | 51 | 27.1 | 174 | 2 | gamma-crystallin 1 |
| 10 | 51 | 27.1 | 174 | 2 | gamma-E-crystallin |
| 11 | 51 | 27.1 | 174 | 2 | gamma-F-crystallin |
| 12 | 51 | 27.1 | 174 | 2 | gamma-crystallin 4 |
| 13 | 51 | 27.1 | 174 | 2 | gamma-crystallin 2 |
| 14 | 50.5 | 26.9 | 313 | 2 | gamma-crystallin |
| 15 | 50 | 26.6 | 467 | 2 | extracellular matr |
| 16 | 49.5 | 26.3 | 564 | 2 | hypothetical prote |
| 17 | 49.5 | 26.3 | 899 | 2 | C02F5.9 protein - |
| 18 | 49.5 | 26.3 | 902 | 2 | probable retroelem |
| 19 | 49.5 | 26.3 | 949 | 2 | hypothetical prote |
| 20 | 49.5 | 26.3 | 973 | 2 | probable retroelem |
| 21 | 49.5 | 26.3 | 1611 | 2 | hypothetical prote |
| 22 | 49 | 26.1 | 126 | 2 | probable retroelem |
| 23 | 49 | 26.1 | 128 | 2 | CD59 protein - bab |
| 24 | 49 | 26.1 | 248 | 2 | CD59 protein - gre |
| 25 | 49 | 26.1 | 367 | 2 | hypothetical prote |
| 26 | 49 | 26.1 | 851 | 2 | hypothetical prote |
| 27 | 48.5 | 25.8 | 323 | 2 | nc1-1 ZK112.2 prot |
| 28 | 48.5 | 25.8 | 324 | 2 | conserved hypothet |
| 29 | 48.5 | 25.8 | 377 | 2 | probable transmemb |
| | | | | | hypothetical prote |

| | | | | | |
|----|------|------|------|---|--------------------|
| 30 | 48 | 25.5 | 63 | 2 | E64024 |
| 31 | 48 | 25.5 | 248 | 2 | conserved hypothet |
| 32 | 48 | 25.5 | 325 | 2 | hypothetical prote |
| 33 | 48 | 25.5 | 325 | 2 | protein W03D8.9 [i |
| 34 | 48 | 25.5 | 365 | 2 | 5S RNA-binding pro |
| 35 | 48 | 25.5 | 557 | 1 | hypothetical prote |
| 36 | 47.5 | 25.3 | 99 | 2 | hypothetical prote |
| 37 | 47.5 | 25.3 | 289 | 2 | probable GT-1-like |
| 38 | 47.5 | 25.3 | 427 | 2 | probable transposa |
| 39 | 47.5 | 25.3 | 491 | 2 | protein C27A12.6 [|
| 40 | 47.5 | 25.3 | 497 | 2 | protein C27A12.7 [|
| 41 | 47.5 | 25.3 | 761 | 2 | hypothetical prote |
| 42 | 47.5 | 25.3 | 807 | 2 | hypothetical prote |
| 43 | 47.5 | 25.3 | 839 | 1 | probable transposa |
| 44 | 47.5 | 25.3 | 1241 | 2 | hypothetical prote |
| 45 | 47.5 | 25.3 | 1303 | 2 | hypothetical prote |

ALIGNMENTS

RESULT 1

I74320
Gene EHS-2 protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
C:Accession: I74320
R:Horwitz, M.S.; Boyce-Jacino, M.T.; Faras, A.J.
J. Virol. 66, 2170-2179, 1992
A:Title: Novel human endogenous sequences related to human immunodeficiency virus type
A:Reference number: 156825; MUID:92194452; PMID:1548756
A:Accession: I74320
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-54 <RES>
A:Cross-references: GB:M86246; NID:g181990; PID:g553274
C:Genetics:
A:Gene: EHS-2

Query Match 31.6%; Score 59.5; DB 2; Length 54;
Best Local Similarity 52.2%; Pred. No. 0.49;
Matches 12; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

QY 11 QKPSGCMOH---ISCNPPGCRTL 30
DB 10 QAPSGCMQDSFCCSCRINGCULL 32

RESULT 2

T09052
hypothetical protein DBCCR1 - human
C:Species: Homo sapiens (man)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09052
R:Habuchi, T.; Luscombe, M.; Elder, P.A.; Knowles, M.A.
Genomics 48, 277-288, 1998
A:Title: Structure and methylation-based silencing of a gene (DBCCR1) within a candidat
A:Reference number: Z16537; MUID:98207242; PMID:9545632
A:Accession: T09052
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-761 <HAB>

A:Cross-references: EMBL:AF027734; NID:g3041876; PIDN:AAC39691.1; PID:g3041877
A:Experimental source: tissue type: brain; developmental stage: fetal and infant
C:Genetics:
A:Gene: DBCCR1
A:Map position: 9q32-q33
A:Note: IB3089A
C:Superfamily: human hypothetical protein DBCCR1

Query Match 29.3%; Score 55; DB 2; Length 761;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 5 SMKSSHOKPSGWOHISCNP 24
DB 19 SVQPSHQEPAGTDQHVSKF 38

RESULT 3

149617

gamma-F-crystallin - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C:Accession: I49617

R:Lok, S.; Breitman, M.L.; Chelpelesky, A.B.; Piatigorsky, J.; Gold, R.J.; Tsui, L.C.

Mol. Cell. Biol. 5, 2221-2230, 1985

A:Title: Lens-specific promoter activity of a mouse gamma-crystallin gene.

A:Reference number: I49617; MUID:86284663; PMID:3837188

A:Accession: I49617

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-69 <RES>

A:Cross-references: GB:M11039; NID:g192784; PIDN:AAA03227.1; PID:g192785

C:Genetics: 3/3

A:Introns: 3/3

C:Superfamily: beta-crystallin

C:Keywords: duplication

Query Match 27.1%; Score 51; DB 2; Length 69;
Best Local Similarity 30.8%; Pred. No. 7.6;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY 2 FSCSMKSSHOKP-----SGCWO-HISCNFPGCR 28

DB 17 YECSTDSHNLQPYFSCNCSVRVDSGCMWLYEQPNFAGCQ 55

RESULT 4

149618

gamma-F-crystallin - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C:Accession: I49618

R:Goring, D.R.; Breitman, M.L.; Tsui, L.C.

Exp. Eye Res. 54, 785-795, 1992

A:Title: Temporal regulation of six crystallin transcripts during mouse lens development

A:Reference number: I49618; MUID:92324352; PMID:1623964

A:Accession: I49618

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-159 <RES>

A:Cross-references: GB:M64543; NID:g192788; PIDN:AAA53525.1; PID:g567200

C:Superfamily: beta-crystallin

C:Keywords: duplication

Query Match 27.1%; Score 51; DB 2; Length 159;
Best Local Similarity 30.8%; Pred. No. 16;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY 2 FSCSMKSSHOKP-----SGCWO-HISCNFPGCR 28

DB 17 YECSTDSHNLQPYFSCNCSVRVDSGCMWLYEQPNFAGCQ 55

RESULT 5

CYRTG1

gamma-crystallin 1 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 13-Jun-1993 #sequence_revision 13-Jun-1993 #text_change 22-Jun-1999

C:Accession: A02930

R:Moormann, R.J.M.; den Dunnen, J.T.; Bloemendal, H.; Schoenmakers, J.G.G.

Proc. Natl. Acad. Sci. U.S.A. 79, 6876-6880, 1982

A:Title: Extensive intragenic sequence homology in two distinct rat lens gamma-crystallin

A:Reference number: A93934; MUID:83091061; PMID:6294661

A:Accession: A02930

A:Molecule type: mRNA

A:Residues: 1-173 <MOO>

A:Cross-references: GB:J00716; NID:g203634; PIDN:AAA0987.1; PID:g203635

C:Superfamily: beta-crystallin

C:Keywords: duplication; eye lens

F:1-39/Domain: crystallin repeat <GK1>

F:40-82/Domain: crystallin repeat <GK2>

F:87-127/Domain: crystallin repeat <GK3>

F:128-167/Domain: crystallin repeat <GK4>

Query Match 27.1%; Score 51; DB 1; Length 173;

Best Local Similarity 30.8%; Pred. No. 17;

Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY 2 FSCSMKSSHOKP-----SGCWO-HISCNFPGCR 28

DB 16 YECSTDSHNLQPYFSCNCSVRVDSGCMWLYEQPNFTGCQ 54

RESULT 6

S04266

gamma-crystallin IV - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999

C:Accession: S04266; C60890

R:White, H.E.; Driessen, H.P.C.; Slingsby, C.; Moss, D.S.; Lindley, P.F.

J. Mol. Biol. 207, 217-235, 1989

A:Title: Packing interactions in the eye-lens. Structural analysis, internal symmetry

A:Reference number: S04265; MUID:89293855; PMID:2738925

A:Accession: S04266

A:Molecule type: protein

A:Residues: 1-173 <WHI>

R:Chiodi, S.H.; Azari, P.; Himmel, M.E.

J. Protein Chem. 7, 67-80, 1988

A:Title: Physicochemical characterization of gamma-crystallins from bovine lens-hydrod

A:Reference number: A60890; MUID:89351571; PMID:3255364

A:Accession: C60890

A:Molecule type: protein

A:Residues: 1-25 <CHI>

A:Note: 14-His, 15-Arg, 22-Cys, 23-Pro, and 24-Asp were also found and may indicate co

C:Superfamily: beta-crystallin

C:Keywords: duplication; eye lens

Query Match 27.1%; Score 51; DB 2; Length 173;

Best Local Similarity 30.8%; Pred. No. 17;

Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY 2 FSCSMKSSHOKP-----SGCWO-HISCNFPGCR 28

DB 16 YECSTDSHNLQPYFSCNCSVRVDSGCMWLYEQPNFTGCQ 54

RESULT 7

CYMSG2

gamma-crystallin 2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999

C:Accession: A02931

R:Breitman, M.L.; Lok, S.; Wistow, G.; Piatigorsky, J.; Treton, J.A.; Gold, R.J.M.; Ts

Proc. Natl. Acad. Sci. U.S.A. 81, 7762-7766, 1984

A:Title: gamma-crystallin family of the mouse lens: structural and evolutionary relation

A:Reference number: A94021; MUID:85088487; PMID:6096855

A:Accession: A02931

A:Molecule type: mRNA

A:Residues: 1-174 <BRE>

A:Cross-references: GB:K02584; NID:g192786; PIDN:AAA03228.1; PID:g309198

C:Comment: There are at least seven different gamma crystallins identified in mouse lei

C:Superfamily: beta-crystallin

C:Keywords: duplication; eye lens

F:2-40/Domain: crystallin repeat <GK1>

F:41-83/Domain: crystallin repeat <GK2>

F:88-128/Domain: crystallin repeat <GK3>

F:129-168/Domain: crystallin repeat <GK4>

```

Query Match      27.1%; Score 51; DB 1; Length 174;
Best Local Similarity 30.8%; Pred. No. 17;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY  2 FSCSMKSSHQKP-----SGCWQ-HISCNFPFPCR 28
Db   17 YECSTDHSLNLPYFRCNSVRVDSGCWMLYEQPNFTGCQ 55

RESULT 8
CYMSG1
C:Species: Mus musculus (house mouse)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999
C:Accession: A02932
R:Breitman, M.L.; Lok, S.; Wistow, G.; Piatigorsky, J.; Treton, J.A.; Gold, R.J.M.; Tsui
Proc. Natl. Acad. Sci. U.S.A. 81, 7762-7766, 1984
A:Title: gamma-crystallin family of the mouse lens: structural and evolutionary relations
A:Reference number: A94021; MUID:85088487; PMID:6096855
A:Accession: A02932
A:Molecule type: mRNA
A:Residues: 1-174 <BRE>
A:Cross-references: GB:K02583; NID:q192778; PIDN:AAA37475.1; PID:q309197
C:Comment: There are at least seven different gamma crystallins identified in mouse lens
C:Keywords: duplication; eye lens
F:2-40/Domain: crystallin repeat <GK1>
F:41-83/Domain: crystallin repeat <GK2>
F:88-128/Domain: crystallin repeat <GK3>
F:129-168/Domain: crystallin repeat <GK4>

Query Match      27.1%; Score 51; DB 1; Length 174;
Best Local Similarity 30.8%; Pred. No. 17;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY  2 FSCSMKSSHQKP-----SGCWQ-HISCNFPFPCR 28
Db   17 YECSTDHSLNLPYFRCNSVRVDSGCWMLYEQPNFTGCQ 55

RESULT 9
S26811
gamma-B-crystallin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S26811
R:Werner, T.
submitted to the EMBL Data Library, February 1991
A:Reference number: S26811
A:Accession: S26811
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-174 <WER>
A:Cross-references: EMBL:X57855; NID:g51061; PIDN:CAA40990.1; PID:g51062
C:Genetics:
A:Introns: 3/3; 84/3
C:Superfamily: beta-crystallin
C:Keywords: duplication

Query Match      27.1%; Score 51; DB 2; Length 174;
Best Local Similarity 30.8%; Pred. No. 17;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY  2 FSCSMKSSHQKP-----SGCWQ-HISCNFPFPCR 28
Db   17 YECSTDHSLNLPYFRCNSVRVDSGCWMLYEQPNFTGCQ 55

RESULT 10
JS0596
gamma-B-crystallin - mouse
C:Species: Mus musculus (house mouse)

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C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Nov-1997
C:Accession: JS0596; S18835
R:Graw, J.; Coban, I.; Liebststein, A.; Werner, T.
Gene.104, 265-270, 1991
A:Title: Murine gamma E-crystallin is distinct from murine gamma 2-crystallin.
A:Reference number: JS0596; MUID:92009223; PMID:1916296
A:Accession: JS0596
A:Molecule type: DNA
A:Residues: 1-174 <GRA>
A:Cross-references: EMBL:X57855
A>Note: this sequence differs two residues from that of rat
C:Genetics:
A:Gene: gamma-E-cry
A:Introns: 3/3; 84/3
C:Superfamily: beta-crystallin
C:Keywords: duplication

Query Match      27.1%; Score 51; DB 2; Length 174;
Best Local Similarity 30.8%; Pred. No. 17;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY  2 FSCSMKSSHQKP-----SGCWQ-HISCNFPFPCR 28
Db   17 YECSTDHSLNLPYFRCNSVRVDSGCWMLYEQPNFTGCQ 55

RESULT 11
E24060
gamma-crystallin 4-1 - rat
N:Alternate names: gamma-F-crystallin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 13-Aug-1999
C:Accession: E24060; I83435
R:den Dunnen, J.T.; Moormann, R.J.M.; Lubsen, N.H.; Schoenmakers, J.G.G.
J. Mol. Biol. 189, 37-46, 1986
A:Title: Concerted and divergent evolution within the rat gamma-crystallin gene family.
A:Reference number: A92927; MUID:87060933; PMID:3783678
A:Accession: E24060
A:Molecule type: DNA
A:Residues: 1-174 <DEN>
A:Cross-references: GB:M19359; GB:M19357; GB:M19354; NID:g203636; PIDN:AAA40988.1; PID:
R:den Dunnen, J.T.; van Neck, J.W.; Cremers, F.P.M.; Lubsen, N.H.; Schoenmakers, J.G.G.
Gene 78, 201-213, 1989
A:Title: Nucleotide sequence of the rat gamma-crystallin gene region and comparison wit
A:Reference number: I60312; MUID:89378747; PMID:2777080
A:Accession: I83435
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-174 <RES>
A:Cross-references: GB:M19357; NID:g203636; PIDN:AAA40988.1; PID:g203637
C:Genetics:
A:Introns: 3/3; 84/3
C:Superfamily: beta-crystallin
C:Keywords: duplication

Query Match      27.1%; Score 51; DB 2; Length 174;
Best Local Similarity 30.8%; Pred. No. 17;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY  2 FSCSMKSSHQKP-----SGCWQ-HISCNFPFPCR 28
Db   17 YECSTDHSLNLPYFRCNSVRVDSGCWMLYEQPNFTGCQ 55

RESULT 12
D24060
gamma-crystallin 2-2 - rat
N:Alternate names: gamma-D-crystallin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 13-Aug-1999
C:Accession: D24060; I83433; S60744
R:den Dunnen, J.T.; Moormann, R.J.M.; Lubsen, N.H.; Schoenmakers, J.G.G.
J. Mol. Biol. 189, 37-46, 1986

```

A;Title: Concerted and divergent evolution within the rat gamma-crystallin gene family.
A;Reference number: A92927; MUID:87060933; PMID:3783678
A;Accession: D24060
A:Molecule type: DNA
A;Residues: 1-174 <EN>
A;Cross-references: GB:M19359; NID:g203626; PIDN:AAA40984.1; PID:g203630; GB:M19354; GB:R;Den Dunnen, J.T.; van Neck, J.W.; Cremers, F.P.M.; Lubsen, N.H.; Schoenmakers, J.G.G.
Gene 78, 201-213, 1989
A;Title: Nucleotide sequence of the rat gamma-crystallin gene region and comparison with A;Reference number: I60312; MUID:89378747; PMID:2777080
A;Accession: I83433
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-174 <RES>
A;Cross-references: GB:M19359; NID:g203626; PIDN:AAA40984.1; PID:g203630 Biochimie 76, 398-403, 1994
A;Title: High level expression of rat gamma-D-crystallin in Escherichia coli.
A;Reference number: S60744; MUID:95151850; PMID:7849105
A;Accession: S60744
A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-174 <OOK>
A;Cross-references: EMBL:X57169; NID:g929827; PIDN:CAA40458.1; PID:g929828 C;Genetics:
A;Introns: 3/3; 84/3
C;Superfamily: beta-crystallin
C;Keywords: duplication

Query Match 27.1%; Score 51; DB 2; Length 174;
Best Local Similarity 30.8%; Pred.No. 17;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY 2 FSCSMKSSHOKP-----SGCWQ-HISCNFPGCR 28
DB 17 YECSTHSNLQPFSCRNSRVDSGCWMLYEQPNFTGCC 55
:::|::|
|||::|::|

RESULT 13
I56381
gamma-crystallin - rat
N;Alternate names: gamma-E-crystallin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
C;Accession: I56381; I83434
R;Moormann, R.J.; den Dunnen, J.T.; Mulleners, L.; Andreoli, P.; Bloemendal, H.; Schoenmakers, J.G.G.
J. Mol. Biol. 171, 353-368, 1983
A;Title: Strict co-linearity of genetic and protein folding domains in an intragenically duplicated gene.
A;Reference number: I56381; MUID:94114867; PMID:6319707
A;Accession: I56381
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-174 <RES>
A;Cross-references: EMBL:X00271; NID:g56193; PIDN:CAA35073.1; PID:g295917
R;Den Dunnen, J.T.; van Neck, J.W.; Cremers, F.P.M.; Lubsen, N.H.; Schoenmakers, J.G.G.
Gene 78, 201-213, 1989
A;Title: Nucleotide sequence of the rat gamma-crystallin gene region and comparison with A;Reference number: I60312; MUID:89378747; PMID:2777080
A;Accession: I83434
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-174 <RED>
A;Cross-references: GB:M19359; NID:g203626; PIDN:AAA40985.1; PID:g203631 C;Genetics:
A;Introns: 3/3; 84/3
C;Superfamily: beta-crystallin
C;Keywords: duplication

Query Match 27.1%; Score 51; DB 2; Length 174;
Best Local Similarity 30.8%; Pred.No. 17;
Matches 12; Conservative 5; Mismatches 10; Indels 12; Gaps 2;

QY 2 FSCSMKSSHOKP-----SGCWQ-HISCNFPGCR 28

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